

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:59:04 ; Search time 48 Seconds  
(without alignments)

2576.112 Million cell updates/sec

Title: US-09-983-000A-20

Perfect score: 2342

Sequence: 1 MRTLPLPALLTCWLLAPVNS.....LQHRGSRAGSFLQTETSVI 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2342	100.0	438	10	US-09-983-000A-20
2	2327	99.4	438	14	US-10-157-031-237
3	2327	99.4	438	14	US-10-225-567A-471
4	2321	99.1	438	11	US-09-826-509-581
5	1153.5	49.3	467	9	US-09-935-371-19
6	1151.5	49.2	485	9	US-09-935-371-17
7	1150	49.1	468	15	US-10-292-798-638
8	1150	49.1	525	9	US-09-935-371-23
9	1150	49.1	525	13	US-10-044-722-3
10	1150	49.1	525	14	US-10-225-567A-231
11	1150	49.1	525	15	US-10-295-027-276
12	1144.5	48.9	468	9	US-09-935-371-22
13	1144	48.8	468	11	US-09-826-509-553
14	1143.5	48.8	448	9	US-09-935-371-18
15	1141.5	48.7	448	9	US-09-935-371-16
					Sequence 20, Appl
					Sequence 27, App
					Sequence 471, App
					Sequence 581, App
					Sequence 19, Appl
					Sequence 17, Appl
					Sequence 638, App
					Sequence 23, Appl
					Sequence 3, Appl
					Sequence 231, App
					Sequence 276, App
					Sequence 22, Appl
					Sequence 553, App
					Sequence 18, Appl
					Sequence 16, Appl

16	1129.5	48.2	495	9	US-09-935-371-21	Sequence 21, Appl
17	1127.5	48.1	513	9	US-09-935-371-15	Sequence 15, Appl
18	1126.5	48.1	552	9	US-09-935-371-27	Sequence 27, Appl
19	1126	48.1	553	9	US-09-935-371-25	Sequence 25, Appl
20	1126	48.1	553	9	US-09-935-371-29	Sequence 29, Appl
21	1121	47.9	475	9	US-09-935-371-26	Sequence 26, Appl
22	1120.5	47.8	476	9	US-09-935-371-24	Sequence 24, Appl
23	1120.5	47.8	476	9	US-09-935-371-28	Sequence 28, Appl
24	1119.5	47.8	476	9	US-09-935-371-20	Sequence 20, Appl
25	1117.5	47.7	476	9	US-09-935-371-14	Sequence 14, Appl
26	1064.5	45.5	1324	9	US-09-935-371-56	Sequence 56, Appl
27	1035.5	44.2	457	14	US-10-225-567A-469	Sequence 469, App
28	1035.5	44.2	457	15	US-10-292-798-618	Sequence 618, App
29	1029.5	44.0	457	11	US-09-826-509-579	Sequence 579, App
30	1018	43.5	495	15	US-10-295-027-875	Sequence 875, App
31	1004.5	42.9	440	14	US-10-225-567A-310	Sequence 310, App
32	1003.5	42.8	440	12	US-10-398-454-3	Sequence 3, Appli
33	1003.5	42.8	440	12	US-10-398-455-3	Sequence 2, Appli
34	1003.5	42.8	440	15	US-10-292-798-608	Sequence 608, App
35	1003.5	42.8	440	15	US-10-051-874-64	Sequence 64, Appl
36	1003.5	42.8	440	15	US-10-051-874-65	Sequence 65, Appl
37	1003.5	42.8	440	16	US-10-398-448-3	Sequence 3, Appli
38	998.5	42.6	440	11	US-09-826-509-567	Sequence 567, App
39	997.5	42.6	440	15	US-10-051-874-66	Sequence 66, Appl
40	997.5	42.6	449	15	US-10-051-874-68	Sequence 68, Appl
41	992.5	42.4	440	15	US-10-051-874-67	Sequence 67, Appl
42	880.5	41.9	421	15	US-10-051-874-10	Sequence 10, Appl
43	881.5	37.6	423	15	US-10-292-798-640	Sequence 640, App
44	879.5	37.6	423	14	US-10-147-087-4	Sequence 4, Appli
45	879.5	37.6	423	14	US-10-225-567A-142	Sequence 142, App

#### ALIGNMENTS

#### RESULT 1

US-09-983-000A-20  
Sequence 20, Application US/09983000A  
Publication No. US20030118585A1

GENERAL INFORMATION:  
APPLICANT: AGY Therapeutics

APPLICANT: Melcher, Thorsten

APPLICANT: Mueller, Sabine

APPLICANT: Chin, Daniel

TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZ

FILE REFERENCE: 263/180 -- PRAGLEMAN -- AGY

CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 438

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)..(23)

OTHER INFORMATION: Potential

NAME/KEY: GENE

LOCATION: (1)..(438)

OTHER INFORMATION: Vasoactive Intestinal Peptide Receptor 2

NAME/KEY: CHAIN

LOCATION: (24)..(438)

OTHER INFORMATION: Vasoactive Intestinal Polypeptide Receptor 2

NAME/KEY: DOMAIN

LOCATION: (24)..(126)

OTHER INFORMATION: 1 (Potential)

NAME/KEY: TRANSMEM

LOCATION: (127)..(151)

OTHER INFORMATION: 1 (Potential)

NAME/KEY: DOMAIN

LOCATION: (152)..(158)

OTHER INFORMATION: Cytoplasmic (potential)  
 NAME/KEY: TRANSMEM  
 LOCATION: (159)..(178)  
 OTHER INFORMATION: 2 (Potential)  
 NAME/KEY: DOMAIN  
 LOCATION: (179)..(203)  
 OTHER INFORMATION: Extracellular (Potential)  
 NAME/KEY: TRANSMEM  
 LOCATION: (204)..(227)  
 OTHER INFORMATION: 3 (Potential)  
 NAME/KEY: DOMAIN  
 LOCATION: (228)..(240)  
 OTHER INFORMATION: Cytoplasmic (Potential)  
 NAME/KEY: TRANSMEM  
 LOCATION: (241)..(262)  
 OTHER INFORMATION: 4 (Potential)  
 NAME/KEY: DOMAIN  
 LOCATION: (263)..(279)  
 OTHER INFORMATION: Extracellular (Potential)  
 NAME/KEY: TRANSMEM  
 LOCATION: (280)..(303)  
 OTHER INFORMATION: 5 (Potential)  
 NAME/KEY: DOMAIN  
 LOCATION: (304)..(328)  
 OTHER INFORMATION: Cytoplasmic (Potential)  
 NAME/KEY: TRANSMEM  
 LOCATION: (329)..(348)  
 OTHER INFORMATION: 6 (Potential)  
 NAME/KEY: DOMAIN  
 LOCATION: (349)..(360)  
 OTHER INFORMATION: Extracellular (Potential)  
 NAME/KEY: TRANSMEM  
 LOCATION: (361)..(380)  
 OTHER INFORMATION: 7 (Potential)  
 NAME/KEY: DOMAIN  
 LOCATION: (381)..(438)  
 OTHER INFORMATION: Cytoplasmic (potential)  
 NAME/KEY: CARBOHYD  
 LOCATION: (58)..(58)  
 OTHER INFORMATION: N-linked (GLCNAC...) (Potential)  
 NAME/KEY: CARBOHYD  
 LOCATION: (88)..(88)  
 OTHER INFORMATION: N-linked (GLCNAC...) (Potential)  
 NAME/KEY: CARBOHYD  
 LOCATION: (92)..(92)  
 OTHER INFORMATION: N-linked (GLCNAC...) (Potential)

US-09-983-000A-20

Query Match  
 Best Local Similarity 100.0%; Score 2342; DB 10; Length 438;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
 QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120  
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120  
 QY 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180  
 DB 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180  
 QY 181 DVLSSSTGLHCPDPSPSSWGCKLSLVFLQYICIMANFFWLLVEGLYHHTLVAMLPERRC 240  
 DB 181 DVLSSSTGLHCPDPSPSSWGCKLSLVFLQYICIMANFFWLLVEGLYHHTLVAMLPERRC 240  
 QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIYNFVLF 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIYNFVLF 300  
 QY 301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

DB 301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
 QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 DB 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 QY 421 FHRGSAQSFLOTETSVI 438  
 DB 421 FHRGSAQSFLOTETSVI 438

## RESULT 2

US-10-157-031-237  
 ; Sequence 237, Application US/10157031  
 ; Publication No. US20030108890A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baranova, A. V.  
 ; APPLICANT: Yankovsky, N. K.  
 ; APPLICANT: Kozlov, A. P.  
 ; APPLICANT: Lobashev, A. V.  
 ; APPLICANT: Krukovskaya, L. L.  
 ; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences  
 ; FILE REFERENCE: 2760-103  
 ; CURRENT APPLICATION NUMBER: US/10/157,031  
 ; NUMBER OF SEQ ID NOS: 415  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 237  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-157-031-237

Query Match  
 Best Local Similarity 99.4%; Score 2327; DB 14; Length 438;  
 Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
 QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120  
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120  
 QY 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180  
 DB 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNYIHLNLFSLFIRALSVLVKD 180  
 QY 181 DVLSSSTGLHCPDPSPSSWGCKLSLVFLQYICIMANFFWLLVEGLYHHTLVAMLPERRC 240  
 DB 181 DVLSSSTGLHCPDPSPSSWGCKLSLVFLQYICIMANFFWLLVEGLYHHTLVAMLPERRC 240  
 QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIYNFVLF 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIIYNFVLF 300  
 QY 301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
 QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 DB 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 QY 421 FHRGSAQSFLOTETSVI 438  
 DB 421 FHRGSAQSFLOTETSVI 438

## RESULT 3

US-10-225-567A-471

```
; Sequence 471, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 471
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-471

Query Match          99.4%; Score 2327; DB 14; Length 438;
Best Local Similarity 99.3%; Pred. No. 7.3e-216;
Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQBEETKCAELLRSQTEKHKACSGVNDIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQBEETKCTELLRSQTEKHKACSGVNDIT 60
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDCGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDCGYSDPEDESKI 120
QY 121 TFYLKAIYTLGVSLSMSLATGSIILCLFRKLHCTRNHYHLNLFSLFIRALSIVLKD 180
Db 121 TFYLKAIYTLGVSLSMSLATGSIILCLFRKLHCTRNHYHLNLFSLFIRALSIVLKD 180
QY 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNFVFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNFVFI 300
QY 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSIKYQLFE 360
Db 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSIKYQLFE 360
QY 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
Db 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRASRAQSFLOTETSVI 438

RESULT 4
US-09-826-509-581
; Sequence 581, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent in version 2.1
; SEQ ID NO 581
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-581

Query Match          99.1%; Score 2321; DB 11; Length 438;
Best Local Similarity 99.1%; Pred. No. 2.8e-215;
Matches 434; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQBEETKCAELLRSQTEKHKACSGVNDIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPCRFHLIEQBEETKCTELLRSQTEKHKACSGVNDIT 60
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Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDCGYSDPEDESKI 120
QY 121 TFYLKAIYTLGVSLSMSLATGSIILCLFRKLHCTRNHYHLNLFSLFIRALSIVLKD 180
Db 121 TFYLKAIYTLGVSLSMSLATGSIILCLFRKLHCTRNHYHLNLFSLFIRALSIVLKD 180
QY 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLOYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNFVFI 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNFVFI 300
QY 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSIKYQLFE 360
Db 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSIKYQLFE 360
QY 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
Db 361 LCLGSFQGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLQ 420
QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRASRAQSFLOTETSVI 438

RESULT 5
US-09-935-371-19
; Sequence 19, Application US/09935371
; Patent No. US20020155533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Masuda, Yasushi
; APPLICANT: Kitada, Chieko
; APPLICANT: Ishibashi, Yoshihiro
; APPLICANT: Hosoya, Masaki
; APPLICANT: Ogi, Kazuhiro
; APPLICANT: Miyamoto, Yasunori
; APPLICANT: Habata, Yugo
; APPLICANT: Shimamoto, No. US20020155533A1
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-935-371-19

Query Match 49.3%; Score 1153.5; DB 9; Length 467;
Best Local Similarity 49.7%; Pred. No. 1.7e-102;
Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCWLLAPVNSHPCEHFLEIQEBETKCAEL-----LRSQTEKHKACSGVMDNITCWR 63
Db 9 LTALLPVAIAHSDCIF---KKGQAMCLEIQRANDLMLGNSSPGCGMWDNITCWK 64

QY 64 PANVGETVTPCPKVFNSF-----YSKAGNISKNCTSDGNS 100
Db 65 PAQGVEMVLVSCPVEFRIFNPQVMTETIGDSGFADSNLSLEITDMGVVGRNCTEDGNS 124

QY 101 TPDFVDAGGYS--PEDESKITFYILVKAITYLGVSVLSMISLATSIIILCFRKLHCTR 158
Db 125 PPFHYFDAGFDYDPESGDQDYLYLVKALYTVGYSTSLATLTAMVILCFRKLHCTR 184

QY 159 NYIHLNLFILRAISVLVKDDVLYSSSGTLCPCDPQSSWVGCKLSLVFLQYCIAMNPF 218
Db 185 NEIHNLFVSMRLAISVFIKWILYAEQDSSHC---FVSTVEKAVWVFFHYCVVSNYP 241

QY 219 WLLVEGLYHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDH 277
Db 242 WLFIEGLYLTLLVETFPFERYFYWYTIIGWGTPTVCVTVNAVRLYFDDAGCDWMDNS 301

QY 278 SVPMWVIRPILISIVNFIPIISIRILLQKLTSPDIVCGNDQSQYKRIAKSTILLILPLF 337
Db 302 TALWVVGKPVVGSIMVNFVLFIGIITILLVQKLPDGMGNGESSIYLRARSTLLILPLF 361

QY 338 GVHYMVAFVPIISISKYILFELCLGSPQGLVAVLYCFNLSEYQCELRKRWGRKCPPT 397
Db 362 GIHYTVFAFSPENVSKRELVELGLGSPQGFVAVLYCFNLGEVQAEIKRWRSWKYNR 421

QY 398 SASRIRYVCGSFSRNGSEGAQOFHGRSAQFLQ 432
Db 422 YFTMDPKRHRPGLASSGVNGGTQLSILSKSSQLR 456

RESULT 6
US-09-935-371-17
; Sequence 17, Application US/09935371
; Patent No. US2002015533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; OHTAKI, Tetsuya
; MASUDA, Yasuhiro
;
; KITADA, Chieko
; ISHIBASHI, Yoshihiro
; HOSoya, Masaki
; OGI, Kazuhiro
; MIYAMOTO, Yasunori
; HABATA, Yugo
; SHIMAMOTO, No. US2002015533A1
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-935-371-17

Query Match 49.2%; Score 1151.5; DB 9; Length 485;
Best Local Similarity 48.6%; Pred. No. 2.8e-102;
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;

QY 1 MRTLPPALLTCWLLAPVNSHPCEHFLEIQEBETKCAEL-----LRSQTEKHKACSG 54
Db 18 MASTAQVSLAALLLPMTAMVHSDCIF---KKGQAMCLEIQRVNDLMLGNSSPGCGP 73

QY 55 VMDNITCWRPANVGETVTPCPKVFNSF-----YSKAGNISK 91
Db 74 MWDNITCWRPANVGETVTPCPKVFNSF-----YSKAGNISK 133

QY 92 NCTSDGSETPDFVDAGGYSDEDES--KITFYILVKAITYLGVSVLSMISLATSIIILC 149
Db 134 NCTEDGSEPPFHYFDAGGFEYSETDQDYLYLVKALYTVGYSTSLVTLTAMVILC 193

QY 150 LFRKLHCTRNYIHLNLFILRAISVLVKDDVLYSSSGTLCPCDPQSSWVGCKLSLVFL 209
Db 194 RFRKLHCTRNYIHLNLFILRAISVLVKDDVLYSSSGTLCPCDPQSSWVGCKLSLVFL 250

QY 210 QYCIAMNPFVLLVEGLYHTLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLED 268
Db 251 HCVVSNYFWLFIEGLYLTLLVETFPFERYFYWYTIIGWGTPTVCVSWAMLELYFDD 310

QY 269 TCGWDNDHNSVPMWVIRPILISIVNFIPIISIRILLQKLTSPDIVCGNDQSQYKRIAK 328
Db 311 TCGWMDNDNTALWWVVGKPVVGSIMVNFVLFIGIITILLVQKLPDGMGNGESSIYLRAR 370

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; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 276
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-276

Query Match 49.1%; Score 1150; DB 15; Length 525;
Best Local Similarity 48.2%; Pred. No. 4.4e-102;
Matches 225; Conservative 68; Mismatches 118; Indels 56; Gaps 7;

QY 12 CW-----LLAPVNSHPECRFHELEQBEETKCAELLRSQTE-----K 48
Db 52 CWPRSVAGVVHVSIAALLLPAMHSDCIF----KKEQAMCLEKIQORANELMGFND 107
QY 49 HKACSGVWDNITCWPRANVGTVTVPCKVFSNF-----YSK 85
Db 108 SPGCPGMDNITCWKPAHVGEMVLVSCPELFRIENPQVWETETIGESDFGDSNLSLD 167
QY 86 AGNISKNCTSDGSETFPDFVADGYSDBEDS--KITFYILVKAIYTLGYSVLSMSIAT 143
Db 168 MGVSVRNCTEDGWSPEPFPHYFDACGDEYBSETGDQDYVYLSVKALYTVGSTSLVLT 227
QY 144 GSIILCLFRKLHCTRNVIHLNLSFTILRAISVLVKDDVLYSSGTHLCHDPQSPSWGCK 203
Db 228 AMVILCRFKLHCTRNFIHNLVFSVFLRAISVFIKDWILYAEQDSNHC---FISTVECK 284
QY 204 LSLVFLQYCIANPFWLLVGLYLHTLLV--AMLPFRRCFLAYLLIGWLPVCIQAWTAA 262
Db 285 AVMVFFHYCVSVYFWLFIQGLYLFTLLVETFFPERYFVWYIILGTTTCVTVWATL 344
QY 263 RLYLEDGCDWTDNDHSPVWVIRIPILISIVNVLVFIIRILLQKLTSPDVGNDSQ 322
Db 345 RLYPDDTGCWDMNDSTALWVVIKGPVVGSIWNVFLFIIIVILVQLQSPDMGNESSI 404
QY 323 YKRLAKSTLLILPLFGVHYVWVAVFPIISISKYQLFELCLGSPQGLVAVLYCFINSEV 382
Db 405 YLRJARSTLLILPLFGIHYTVAFSPENVSKRELVEFGLGSPQGFVAVLYCFINLGEV 464
QY 383 QCELKRWRSRCPTPSASRYRVCGSSFRNSGSEGALQPHRGSRAQS 429
Db 429 QCELKRWRSRCPTPSASRYRVCGSSFRNSGSEGALQPHRGSRAQS 429

Db 465 QAEIKRWRSWKVNRYPVAVDFKRRHPSLASSGVNGGTQLSILSKSS 511

RESULT 12
US-09-935-371-22
; Sequence 22, Application US/09935371
; Patent No. US20020155533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; OHTAKI, Tetsuya
; MASUDA, Yasushi
; KITADA, Chieko
; ISHIBASHI, Yoshihiro
; HOSoya, Masaaki
; OGI, Kazuhiro
; MIYAMOTO, Yasunori
; HABATA, Yugo
; SHIMAMOTO, No. US20020155533A110
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-935-371-22

Query Match 48.9%; Score 1144.5; DB 9; Length 448;
Best Local Similarity 50.1%; Pred. No. 1.2e-101;
Matches 221; Conservative 67; Mismatches 114; Indels 39; Gaps 6;

QY 21 IHPECRFHELEQBEETKCAELLRSQTE-----XSKAGNISKNCTSDGSETFPDFVADCGY 111
Db 1 MHSDCIF----KKEQAMCLEKIQORANELMGFNDSPGCPGMDNITCWKPAHVGEMVLVS 56
QY 75 CPKVFNSF-----YSKAGNISKNCTSDGSETFPDFVADCGY 111
Db 57 CPFLRIFNPQVWETETIGESDFGDSNLSLDGMSVSRNCTEDGWSPEPFPHYFDACGF 116
QY 112 SDPEDES--KITFYILVKAIYTLGYSVLSMSIATGSIILCLFRKLHCTRNVIHLNLSF 169
Db 117 DEYSETGDDQDYVYLSVKALYTVGSTSLVLTAMVILCRFKLHCTRNFIHNLVFSF 176
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```
Db 57 CPEVFRIFPDQVWMTETIGDGFADNSLEITDMGVVGRNCTEDGWSEPPHYFDACGF 116
QY 112 SD--PEDESKITFYILVKAITYTGYSVLSLATSILCLFRKLHCTRYIHLNLFSP 169
Db 117 DVEFESGDQDYLYSVKALYTVGYSTLATTAMVILCRFKLHCTRNFIHMLFVSF 176
QY 170 ILRAISVLVDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCIAMNFFWLLVGLYLHT 229
Db 177 MLRAISVFIKDWILYAEQDSHC---FVSTVECKANVWFHYCVSVYFWLFI EGLYLT 233
QY 230 LLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDTNDHSPVWVIRIPI 288
Db 234 LLVETFPERRFYFYIIGWGTPTVCVTVMAVRLYFDAGCWMNDSTALMWVVKGPV 293
QY 289 LISIIVNVLFIISIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFP 348
Db 294 VGSIMVNFVLFIGHIILVQKLOSPDMGNESSIYLRLARSTLLIPLFGIHYTVFAFSP 353
QY 349 ISISSKYQILFELCLGSGFQGLVAVLYCFLNSEVQCBLKRWKRSRCPTPSASRDYRVCGS 408
Db 354 ENVSKEERLVFELGLGSGFQGVVAVLYCFLNGEVAQAEIKRWKRSWKVRYFTWDFKRRHP 413
QY 409 SFSRNGSEGALQPHRGSRAQSLQ 432
Db 414 SLASSGVNGGTQLSILSKSSQLR 437
```

## RESULT 15

US-09-935-371-16

; Sequence 16, Application US/09935371

; Patent No. US2002015533A1

; GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo

; OHTAKI, Tetsuya

; MASUDA, Yasushi

; KITADA, Chieko

; ISHIBASHI, Yoshihiro

; HOSoya, Masaki

; OGI, Kazuhiro

; MIYAMOTO, Yasunori

; HABATA, Yugo

; SHINAMOTO, No. US2002015533A110

; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING

; SAID PROTEIN, AND USE THEREOF

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &amp;

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/935,371

; FILING DATE: 22-Aug-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/201,474

; FILING DATE: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: RESNICK, David S.

; REGISTRATION NUMBER: 34235

; REFERENCE/DOCKET NUMBER: 44168-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

```
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-935-371-16
```

Query Match 48.7%; Score 1141.5; DB 9; Length 448;

Best Local Similarity 49.9%; Pred. No. 2.4e-101;

Matches 220; Conservative 68; Mismatches 114; Indels 39; Gaps 6;

```
QY 21 IHPECRPHLEIQEETKCAEL-----LRSQTEKHKACSGVNDNITCWRPANGETVTP 74
Db 1 MHSDCLF---KKEQAMCLEKIQRVNDLMGLNDSPPCGPWNDNITCWKPAHUGEWLVLS 56
QY 75 CPKVFSNF-----YSKAGNISKNCTSDGWSSETFPDFVDACGY 111
Db 57 CPSELRIFNPDQVWETETIGEGFADSKSLDLSMRVVSRNCTEDGWSEPPHYFDACGF 116
QY 112 SDPEDES--KITFYILVKAITYTGYSVLSLATSILCLFRKLHCTRYIHLNLFSP 169
Db 117 EYSESETGDQDYLYSVKALYTVGYSTLVTLTAMVILCRFKLHCTRNFIHMLFVSF 176
QY 170 ILRAISVLVDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCIAMNFFWLLVGLYLHT 229
Db 177 MLRAISVFIKDWILYAEQDSNHC---FVSTVECKANVWFHYCVSVYFWLFI EGLYLT 233
QY 230 LLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDTNDHSPVWVIRIPI 288
Db 234 LLVETFPERRFYFYIIGWGTPTVCVTVMAVRLYFDAGCWMNDSTALMWVVKGPV 293
QY 289 LISIIVNVLFIISIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFP 348
Db 294 VGSIMVNFVLFIGHIILVQKLOSPDMGNESSIYLRLARSTLLIPLFGIHYTVFAFSP 353
QY 349 ISISSKYQILFELCLGSGFQGLVAVLYCFLNSEVQCBLKRWKRSRCPTPSASRDYRVCGS 408
Db 354 ENVSKEERLVFELGLGSGFQGVVAVLYCFLNGEVAQAEIKRWKRSWKVRYFTWDFKRRHP 413
QY 409 SFSRNGSEGALQPHRGSRAOS 429
Db 414 SLASSGVNGGTQLSILSKSSS 434
```

Search completed: June 22, 2004, 09:05:00

Job time : 50 secs

The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h15571. h15571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory disorders including asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, graft versus host disease, cystic fibrosis and, in

CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
 CC in the production of antibodies against GPCR and in assays to identify  
 CC modulators (agonists and antagonists) of GPCR expression and activity.  
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
 CC used as diagnostic agents for detecting the presence of GPCR polypeptides  
 CC in samples

XX SQ Sequence 438 AA;

Query Match 100.0%; Score 2342; DB 4; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-226;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120  
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120

QY 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNTHLNLFLSFIILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNTHLNLFLSFIILRAISVLVKD 180

QY 181 DVLVSSSGTLHCPDQPSWVGCKLSLFLQYICIMANFPWLLVEGLYHTLIVAMLPERRC 240  
 DB 181 DVLVSSSGTLHCPDQPSWVGCKLSLFLQYICIMANFPWLLVEGLYHTLIVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSVPMWVIRIPILISIVNFVLI 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSVPMWVIRIPILISIVNFVLI 300

QY 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCSSFRNGSEGLQ 420  
 DB 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCSSFRNGSEGLQ 420

QY 421 FHRGSAQSFLOTETSVI 438  
 DB 421 FHRGSAQSFLOTETSVI 438

# RESULT 2

ABB79170  
 ID ABB79170 standard; protein; 438 AA.

XX AC ABB79170;

XX DT 07-AUG-2002 (first entry)

XX DE Human VPAC2 receptor protein SEQ ID NO:10.

XX KW VPAC receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;  
 KW vasoactive intestinal peptide; muscle mass regulator; antibacterial;  
 KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;  
 KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;  
 KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;  
 KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.

XX OS Homo sapiens.

XX PN WO200235240-A2.

XX PD 02-MAY-2002.

XX PF 22-OCT-2001; 2001WC-US043882.

XX PR 23-OCT-2000; 2000US-00694519.

XX (PROC ) PROCTER & GAMBLE CO.

XX Isfort RU, Sheldon RU;

XX WPI; 2002-471451/50.

PT Identifying candidate compounds for regulating skeletal muscle mass or  
 PT function by contacting test compound with vasoactive intestinal peptide  
 PT receptors or cell expressing the receptor.

XX Example 1; Page 77-78; 87pp; English.

CC The present invention describes a method for identifying candidate  
 CC compounds (CC) for regulating skeletal muscle mass or function. The  
 CC method involves contacting a test compound (TC) with a vasoactive  
 CC intestinal peptide receptors (VPAC) or cell expressing VPAC receptor and  
 CC determining whether TC binds to VPAC receptor or TC that activates the  
 CC VPAC receptors, where the TC that binds to or activates VPAC is  
 CC identified as CC. The method can be used for identifying CC for  
 CC regulating skeletal mass or function. Other methods from the present  
 CC invention can be used for: identifying CC that prolong or augment the  
 CC activation of VPAC receptor or VPAC receptor signal transduction pathway;  
 CC identifying CC for increasing VPAC receptor expression; identifying CC  
 CC for increasing the expression of vasoactive intestinal peptide (VIP) or a  
 CC VIP analogue; increasing skeletal mass or function in a subject; and for  
 CC treating skeletal muscle atrophy in a subject. A pharmaceutical  
 CC composition comprising a safe and effective amount of a VPAC receptor  
 CC agonist can be used for modulating skeletal muscle atrophy which includes  
 CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,  
 CC broken bones, denervation/nerve damage due to spinal cord injury,  
 CC autoimmune disease, infectious disease, glucocorticoid use for unrelated  
 CC conditions, sepsis due to infection or other causes, nutrient limitation,  
 CC due to illness or starvation, cancer, cachexia, chronic inflammation,  
 CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic  
 CC disorders, e.g., muscular dystrophies, neurodegenerative diseases. The  
 CC present sequence represents a VPAC2 receptor which is given in the  
 CC exemplification of the present invention

XX Sequence 438 AA;

Query Match 100.0%; Score 2342; DB 5; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-226;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60

DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQEBETKCAELLRSQTEKHKACSGWMDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120

DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKI 120

QY 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNTHLNLFLSFIILRAISVLVKD 180

DB 121 TFYILVKAITYLGYSVSLMSLATGSIILCLPRKLHCTRNTHLNLFLSFIILRAISVLVKD 180

QY 181 DVLVSSSGTLHCPDQPSWVGCKLSLFLQYICIMANFPWLLVEGLYHTLIVAMLPERRC 240

DB 181 DVLVSSSGTLHCPDQPSWVGCKLSLFLQYICIMANFPWLLVEGLYHTLIVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSVPMWVIRIPILISIVNFVLI 300

DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSVPMWVIRIPILISIVNFVLI 300

QY 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360

DB 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCSSFRNGSEGLQ 420

DB 361 LCLGSFQGLVAVLYCFINSEVQCELRKWRSCPTPSASRDYRVCSSFRNGSEGLQ 420

```

QY 421 FHRGSAQSFLOTETSVI 438
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 3
AAU31575
ID AAU31575 standard; protein; 439 AA.
XX
AC AAU31575;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #2066.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
*PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 461; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptides. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 439 AA;

Query Match 100.0%; Score 2342; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 1e-226;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLTPALLTCWLLAPVNSHPHCRFHEIQEBETKCAELLRSQTEKHKACSGWQDIT 60
DB 1 MRTLTPALLTCWLLAPVNSHPHCRFHEIQEBETKCAELLRSQTEKHKACSGWQDIT 60

QY 61 CWRPANYGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDSKI 120
DB 61 CWRPANYGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDSKI 120

us-09-983-000a-20.rag
121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFSLRAISVLVKD 180
DB 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFSLFSLRAISVLVKD 180

QY 181 DVLYSSSGTLLHCPDQPSWVGCKLSLVFLOYCINANFFWLLVGLYHLTLVAMLPERRC 240
DB 181 DVLYSSSGTLLHCPDQPSWVGCKLSLVFLOYCINANFFWLLVGLYHLTLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIVNVLFI 300
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIVNVLFI 300

QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360
DB 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPSPASRDYRVCGSSFSRNGSEGALQ 420
DB 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPSPASRDYRVCGSSFSRNGSEGALQ 420

QY 421 FHRGSAQSFLOTETSVI 438
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 4
AAW80308
ID AAW80308 standard; protein; 438 AA.
XX
AC AAW80308;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human PACAP/VIP R-2 receptor amino acid sequence.
XX
KW Human; energy homeostasis peptide hormone receptor; PACAP/VIP R-2;
KW pituitary adenylate cyclase activating polypeptide;
KW vasoactive intestinal polypeptide;
KW cAMP-mediated signal transduction pathway.
XX
XX Homo sapiens.
XX
PN US5831051-A.
XX
PD 03-NOV-1998.
XX
PF 03-OCT-1995; 95US-00538816.
XX
PR 09-MAY-1995; 95US-00437466.
XX
PA (UVRQ ) UNIV ROCKEFELLER.
XX
PI Wei Y, Mojsov S;
XX
DR WPI; 1998-609326/51.
XX
DR N-PSDB; AAV66581.
XX
PT DNA encoding human energy homeostasis peptide hormone receptors - useful
PT for producing e.g. recombinant receptor proteins.
XX
XX Claim 1; Fig 1A-B; 45pp; English.
XX
CC The present sequence represents a human energy homeostasis peptide
CC hormone receptor called PACAP/VIP R-2. Pituitary adenylate cyclase
CC activating polypeptide (PACAP) and vasoactive intestinal polypeptide
CC (VIP) are structurally related proteins with multiple physiological
CC effects. The present receptor is coupled to the cAMP-mediated signal
CC transduction pathway
XX
SQ Sequence 438 AA;

Query Match 99.5%; Score 2331; DB 2; Length 438;
Best Local Similarity 99.5%; Pred. No. 1.3e-225;

```

Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120  
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120

QY 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180

QY 181 DVLYSSTGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP PRRC 240  
 DB 181 DVLYSSTGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP PRRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300

QY 301 SIIRILLOKLTSPDVGNDQSQYKELAKSTLLILPLFGVHYMVFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLOKLTSPDVGNDQSQYKELAKSTLLILPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCSSFSHNGSEGALQ 420  
 DB 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCSSFSHNGSEGALQ 420

QY 421 PHRSGRAQSFLQTETSVI 438  
 DB 421 PHRSGRAQSFLQTETSVI 438

## RESULT 5

\* AAW92972  
 ID AAW92972 standard; protein; 438 AA.  
 XX AC AAW92972;  
 XX 20-MAR-2003 (revised)  
 DT 14-MAY-1999 (first entry)  
 XX Human PACAP/VIP R-2 protein.  
 XX PACAP/VIP R-2; energy homeostasis peptide hormone receptor; VIP;  
 KW pituitary adenylate cyclase; PACAP; vasoactive intestinal peptide;  
 KW PACAP/VIP R2B; detection; modulation; diagnosis; treatment; cancer;  
 KW pre-cancerous lesion; viral infection; metabolic; neuroendocrine;  
 KW neurotransmitter; hormone; disorder; insulin secretion; antidiabetic;  
 KW reproductive function; anticancer; antiviral; PACAP-27; PACAP-38;  
 KW secretin; human.  
 XX OS Homo sapiens.  
 XX PN US9882899-A.  
 XX PD 16-MAR-1999.  
 XX PF 12-MAY-1998; 98US-00076651.  
 PR 09-MAY-1995; 95US-00437466.  
 PR 03-OCT-1995; 95US-00538816.  
 XX (UYRQ ) UNIV ROCKSFELLER.  
 XX Wei Y, Mojsos S;  
 PI WPI; 1999-214065/19.  
 DR N-PSDB; AAX02878.  
 XX New second common pituitary adenylate cyclase activating

PT polypeptide/vasoactive intestinal polypeptides - useful for control of  
 PT energy homeostasis, including insulin secretion.  
 PS Claim 1; Fig 1A-B; 45pp; English.  
 XX This invention describes novel energy homeostasis peptide hormone  
 CC receptors representing a second common pituitary adenylate cyclase  
 CC activating polypeptide/vasoactive intestinal polypeptide R-2 (PACAP/VIP R  
 CC -2) and PACAP/VIP R2B. The products of the invention can be used for  
 CC detection of the presence/expression of the receptors, the modulation of  
 CC expression of the receptors, or the addition of the receptors or their  
 CC fragments can be used to treat or diagnose cancer, pre-cancerous lesions,  
 CC viral infections, or metabolic, neuroendocrine and/or neurotransmitter  
 CC hormone disorders, control energy homeostasis, including insulin  
 CC secretion, and modulate reproductive function. The receptors have  
 CC antidiabetic, anticancer and antiviral activity and are capable of  
 CC binding to PACAP-27, PACAP-38, VIP, and secretin. (Updated on 20-MAR-2003  
 CC to correct PF field.)

SQ Sequence 438 AA;

Query Match 99.5%; Score 2331; DB 2; Length 438;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-225;  
 Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120  
 DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120

QY 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLFRKLHCTRYIHLNLFILRAISVLVKD 180

QY 181 DVLYSSTGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP PRRC 240  
 DB 181 DVLYSSTGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP PRRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNFVFI 300

QY 301 SIIRILLOKLTSPDVGNDQSQYKELAKSTLLILPLFGVHYMVFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLOKLTSPDVGNDQSQYKELAKSTLLILPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCSSFSHNGSEGALQ 420  
 DB 361 LCLGSFQGLVAVLYCFLNSEVQCELCRKRWSRCPTPSASRDYRVCSSFSHNGSEGALQ 420

QY 421 PHRSGRAQSFLQTETSVI 438  
 DB 421 PHRSGRAQSFLQTETSVI 438

## RESULT 6

AAW48122  
 ID AAW48122 standard; protein; 438 AA.  
 XX AC AAW48122;  
 XX 05-MAR-2002 (first entry)  
 DT Human PACAP/VIP R-2 receptor.

XX Human; PACAP/VIP R-2; receptor; antidiabetic; anti-infertility;  
 KW energy homeostasis; peptide hormone; Vasoactive Intestinal Polypeptide;  
 KW Pituitary Adenylate Cyclase Activating Polypeptide; insulin secretion;  
 KW reproductive function; diabetes; reproductive dysfunction; brain;  
 KW adipocytes; pancreas; skeletal muscle; stomach; kidney; heart.



	Matches	436;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	MRTLLPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELLRSQTEKHKACSGWDNIT	60							
Db	1	MRTLLPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELLRSQTEKHKACSGWDNIT	60							
QY	61	CWRPANVGTVTPCPKFVSNEFYSKAGNISKNCTSDGSETFPDFVDACGYSDPEDESKI	120							
Db	61	CWRPANVGTVTPCPKFVSNEFYSKAGNISKNCTSDGSETFPDFVDACGYSDPEDESKI	120							
QY	121	TFYILVKAIYTLGYSVLSMLATGSIIILCLFRKLHCTRNVIHLNLFLSFILRAISVLVKD	180							
Db	121	TFYILVKAIYTLGYSVLSMLATGSIIILCLFRKLHCTRNVIHLNLFLSFILRAISVLVKD	180							
QY	181	DVLYSSSGLTHCDPOPSWGWCKLSLVFLQYCIMANFFWLVEGLYLHTLLVAMLPERRC	240							
Db	181	DVLYSSSGLTHCDPOPSWGWCKLSLVFLQYCIMANFFWLVEGLYLHTLLVAMLPERRC	240							
QY	241	FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWWIRIPILISIIIVNFVLI	300							
Db	241	FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWWIRIPILISIIIVNFVLI	300							
QY	301	SIIIRILOKLTSPDVGGNDOSQYKRLAKSTLILLPLFGVHYMFAVFPISSIKYQLIFE	360							
Db	301	SIIIRILOKLTSPDVGGNDOSQYKRLAKSTLILLPLFGVHYMFAVFPISSIKYQLIFE	360							
QY	361	LCLGSPQGLVAVLYCFLNSEVQCCELKRKWSRCPTTASRDYRVCGSSFERNSEGALQ	420							
Db	361	LCLGSPQGLVAVLYCFLNSEVQCCELKRKWSRCPTTASRDYRVCGSSFERNSEGALQ	420							
QY	421	FHRGSAQSFLQTETSIVI	438							
Db	421	FHRGSAQSFLQTETSIVI	438							
RESULT 8										
ID	ABG27816	standard; protein; 454 AA.								
AC	ABG27816;									
XX	18-FEB-2002	(first entry)								
DE	Novel human diagnostic protein #27807.									
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;									
KW	food supplement; medical imaging; diagnostic; genetic disorder.									
XX	Homo sapiens.									
OS										
XX	WO200175067-A2.									
PN	11-OCT-2001.									
PD	30-MAR-2001; 2001WO-US008631.									
XX	31-MAR-2000; 2000US-00540217.									
PR	23-AUG-2000; 2000US-00649167.									
XX	(HYSE-) HYSEQ INC.									
PA	Drmanac RT, Liu C, Tang YT;									
PI	WPI; 2001-639362/73.									
DR	N-PSDB; AAS92003.									
XX	New isolated polynucleotide and encoded polypeptides, useful in									
PT	diagnostics, forensics, gene mapping, identification of mutations									
PT	responsible for genetic disorders or other traits and to assess									
PT	biodiversity.									
XX	Claim 20; SEQ ID NO 58175; 103pp; English.									
PS	Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;									
KW	FSAD; neutral endopeptidase inhibitor; I:NBP; enkephalinase;									
XX	Human vasoactive intestinal peptide (VIP) receptor subtype, VPAC2.									

KW gynaecological; vasoactive intestinal peptide receptor subtype; VIP;  
 KW VPAC2; endopeptidase-2.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= Signal\_peptide  
 FT Protein 24..438  
 FT /label= Human\_mature\_VPAC2  
 XX EPI097719-A1.  
 PN  
 XX  
 PD 09-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000EP-00309722.  
 XX  
 PR 08-NOV-1999; 99GB-00026437.  
 PR 18-FEB-2000; 2000GB-00004021.  
 PR 26-MAY-2000; 2000GB-00013001.  
 PR 05-JUL-2000; 2000GB-00016563.  
 PR 12-JUL-2000; 2000GB-00017141.  
 XX  
 PA (PFIZ ) PFIZER LTD.  
 PA (PFIZ ) PFIZER INC.  
 XX  
 PI Maw GN, Wayman CP;  
 XX  
 DR WPI; 2001-309880/33.  
 DR N-PSDB; AAD14533.  
 XX  
 PT Treating females suffering from female sexual dysfunction, preferably  
 -PT female sexual arousal dysfunction using a neutral endopeptidase inhibitor  
 PT that potentiates CAMP in female genitalia.  
 XX  
 PS Disclosure; Page 105; 124pp; English.  
 XX  
 CC The present invention relates to a method for treating female sexual  
 CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).  
 CC The method comprising using an agent, an inhibitor of neutral  
 CC endopeptidase (NEP) EC 3.4.24.11 or I:NEP, which is capable of  
 CC potentiating CAMP (which enhances female genital blood flow) in the  
 CC sexual genitalia of the females. NEP is also known as enkephalinase or  
 CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier  
 CC or excipient. The method restores a normal sexual arousal response,  
 CC particularly increased blood flow leading to vaginal, clitoral and labial  
 CC engorgement. This will result in increased vaginal lubrication via plasma  
 CC transduction, increased vaginal compliance and increased genital (e.g.  
 CC vaginal and clitoral) sensitivity. The present sequence is human  
 CC vasoactive intestinal peptide (VIP) receptor subtype, VPAC2 used in the  
 CC method of the invention  
 XX  
 SQ Sequence 438 AA;

Query Match 99.4%; Score 2327; DB 4; Length 438;  
 Best Local Similarity 99.3%; Pred. No. 3.3e-225;  
 Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSHPECRPHLEIQEETKCTELLRSQTEKHKACSGWMDNIT 60  
 QY 61 CWRPANVGETVTPCPKVFNSFYSKAGNISKNCTSDGWSFTFPDVFADAGSYSDPEDESKI 120  
 DB 61 CWRPANVGETVTPCPKVFNSFYSKAGNISKNCTSDGWSFTFPDVFADAGSYSDPEDESKI 120  
 QY 121 TFYILVKAITYLGVSVMLSLATGSIILCLFRKLHCTRNHYHLNLFILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGVSVMLSLATGSIILCLFRKLHCTRNHYHLNLFILRAISVLVKD 180  
 QY 181 DVLVSSSGTLHCPDQPSWVGCKSLVFLQYCIANFFWLLVEGLYHLTLLVAMLPVPRRC 240  
 DB 181 DVLVSSSGTLHCPDQPSWVGCKSLVFLQYCIANFFWLLVEGLYHLTLLVAMLPVPRRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCWDTNDHSPVWVIRIPILISIVNVLFI 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCWDTNDHSPVWVIRIPILISIVNVLFI 300  
 QY 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLILPLFGVHYMVFAVFPISISSKYQIILFE 360  
 DB 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLILPLFGVHYMVFAVFPISISSKYQIILFE 360  
 QY 361 LCLGSFQGLVAVLYCFNLSEVQCELKWKRSRCPPTPSASRDYRVCGSFSGRNGSEGALQ 420  
 DB 361 LCLGSFQGLVAVLYCFNLSEVQCELKWKRSRCPPTPSASRDYRVCGSFSGRNGSEGALQ 420  
 QY 421 FHRGSRQSFLOTETSVI 438  
 DB 421 FHRASRAQSFLQTETSVI 438

## RESULT 10

AAE07925

ID AAE07925 standard; protein; 438 AA.

XX AAE07925;

DT 01-NOV-2001 (first entry)

XX Human vasoactive intestinal peptide (VIP) receptor protein, VPAC2.

XX Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;  
 KW FSAD; neuropeptide Y; NPY; gynaecological; vasoactive intestinal peptide;  
 KW VIP receptor; VPAC2; pituitary adenylate cyclase-activating peptide;  
 KW PACAP; VIP2; helodermin-preferring VIP receptor.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT /label= Signal\_peptide  
 FT Protein 24..438  
 FT /label= Human\_mature\_VPAC2\_protein

XX EPI097718-A1.

XX 09-MAY-2001.

XX 03-NOV-2000; 2000EP-00309720.

XX 08-NOV-1999; 99GB-00026437.

XX 18-FEB-2000; 2000GB-00004021.

XX 26-MAY-2000; 2000GB-00013001.

XX 05-JUL-2000; 2000GB-00016563.

XX 12-JUL-2000; 2000GB-00017141.

XX (PFIZ ) PFIZER LTD.

XX (PFIZ ) PFIZER INC.

XX Maw GN, Wayman CP;

XX WPI; 2001-319199/34.

XX N-PSDB; AAD14523.

XX Treating females suffering from female sexual dysfunction, preferably

XX female sexual arousal dysfunction using a neuropeptide Y inhibitor that

XX potentiates CAMP in female genitalia.

XX Disclosure; Page 143-145; 165pp; English.

XX The patent discloses a method for the treatment of a female suffering

XX from female sexual dysfunction (FSD), preferably female sexual arousal

XX dysfunction (FSAD) by the use of an agent which is an inhibitor of

XX neuropeptide Y (NPY). The agent is capable of potentiating CAMP which

XX enhances female genital (e.g. vaginal or clitoral) blood flow in the

XX sexual genitalia of the female and is optionally admixed with a diluent



CC carrier or excipient. The method restores a normal sexual arousal  
CC response namely, increased blood flow leading to vaginal, clitoral and  
CC labial engorgement. This will result in increased vaginal lubrication via  
CC plasma transduction, increased vaginal compliance and increased genital  
CC (e.g. vaginal and clitoral) sensitivity. The method is used for treating  
CC a female suffering from FSD preferably FSAD. The present sequence is  
CC vasoactive intestinal peptide (VIP) receptor subtype, VPAC2 from human.  
CC VPAC2 is also known as VIP2 or PACAP (pituitary adenylate cyclase-  
CC activating peptide). Human VIP2 was previously known as helodermin-  
CC preferring VIP receptor. VIP is released during pelvic nerve stimulation  
CC or sexual arousal and induces clitoral vasorelaxation via the CAMP  
XX pathway  
XX  
XX Sequence 438 AA;  
XX  
XX Query Match 99.4%; Score 2327; DB 4; Length 438;  
XX Best Local Similarity 99.3%; Pred. No. 3.3e-225;  
XX Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCAELRSQTEKHKACSGVNDIT 60  
XX 1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCTELLRSQTEKHKACSGVNDIT 60  
XX 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSPPEDSKI 120  
XX 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSPPEDSKI 120  
XX 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLFTRAIISVLVKD 180  
XX 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLFTRAIISVLVKD 180  
XX 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240  
XX 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240  
XX 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300  
XX 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300  
XX 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILPLFGVHYMVFAVFPPISSIKYQILFE 360  
XX 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILPLFGVHYMVFAVFPPISSIKYQILFE 360  
XX 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420  
XX 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420  
XX 421 FHRGSAQSFLOTETSVI 438  
XX 421 FHRGSAQSFLOTETSVI 438  
XX  
XX RESULT 11  
XX ID AAB85124  
XX AC AAB85124 standard; protein; 438 AA.  
XX AC AAB85124;  
XX XX  
XX DT 22-AUG-2001 (first entry)  
XX XX  
XX DE Human helodermin-preferring VIP receptor (VIP2/PACAP).  
XX XX  
XX KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;  
XX KW genital; vaginal; clitoral; blood flow; CAMP; phosphodiesterase; PDE;  
XX KW cAMP; medicament; human; vasoactive intestinal peptide; VIP; VIP2; PACAP.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX PN EP1097707-A1.  
XX XX  
XX PD 09-MAY-2001.  
XX XX  
XX PF 03-NOV-2000; 2000EP-00309719.

XX 08-NOV-1999; 99GB-00026437.  
XX 18-FEB-2000; 2000GB-00004021.  
XX 26-MAY-2000; 2000GB-00013001.  
XX 05-JUL-2000; 2000GB-00016563.  
XX 12-JUL-2000; 2000GB-00017141.  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX Maw GN, Wayman CP;  
XX WPI: 2001-383217/41.  
XX N-PSDB; AAF84032.  
XX Novel pharmaceutical composition for treating female sexual dysfunction,  
XX preferably female sexual arousal disorder, comprising an agent capable of  
XX potentiating CAMP in the sexual genitalia of the female.  
XX Disclosure; Page 112-113; 135pp; English.  
XX The invention provides a pharmaceutical composition for treating female  
XX sexual dysfunction (FSD), preferably female sexual arousal disorder  
XX (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow  
XX in a female. The composition comprises an agent capable of potentiating  
XX CAMP in the sexual genitalia of the female. The agent is an inhibitor  
XX (I:PDE) of phosphodiesterase (PDE), which hydrolyzes CAMP (optionally  
XX cAMP). The agent is useful in the manufacture of a medicament for the  
XX treatment of FSD, preferably FSAD, by potentiating CAMP in the sexual  
XX genitalia. It is also useful in the manufacture of a medicament for  
XX enhancing female genital (e.g., vaginal or clitoral) blood flow. The  
XX present sequence represents a human helodermin-preferring VIP (vasoactive  
XX intestinal peptide) receptor (VIP2/PACAP)  
XX  
XX Sequence 438 AA;  
XX  
XX Query Match 99.4%; Score 2327; DB 4; Length 438;  
XX Best Local Similarity 99.3%; Pred. No. 3.3e-225;  
XX Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCAELRSQTEKHKACSGVNDIT 60  
XX 1 MRTLPPALLTCWLLAPVNSIHPECFRHLIEQBEETKCTELLRSQTEKHKACSGVNDIT 60  
XX 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSPPEDSKI 120  
XX 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSPPEDSKI 120  
XX 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLFTRAIISVLVKD 180  
XX 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLFTRAIISVLVKD 180  
XX 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240  
XX 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCYIMANFFWLLVEGLYHLTLVAMLPERRC 240  
XX 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300  
XX 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPWVIRIPILISIVNVLFI 300  
XX 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILPLFGVHYMVFAVFPPISSIKYQILFE 360  
XX 301 SIIRILLQKLTSPDVGNDSQYKRLAKSTLILPLFGVHYMVFAVFPPISSIKYQILFE 360  
XX 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420  
XX 361 LCLGSFQGLVAVLYCFNLSEVOCELKRWKRSRCPFPSASRDYRVCGSSFSRNGSEGALQ 420  
XX 421 FHRGSAQSFLOTETSVI 438  
XX 421 FHRGSAQSFLOTETSVI 438  
XX  
XX RESULT 11  
XX ID AAB85124  
XX AC AAB85124 standard; protein; 438 AA.  
XX AC AAB85124;  
XX XX  
XX DT 22-AUG-2001 (first entry)  
XX XX  
XX DE Human helodermin-preferring VIP receptor (VIP2/PACAP).  
XX XX  
XX KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;  
XX KW genital; vaginal; clitoral; blood flow; CAMP; phosphodiesterase; PDE;  
XX KW cAMP; medicament; human; vasoactive intestinal peptide; VIP; VIP2; PACAP.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX PN EP1097707-A1.  
XX XX  
XX PD 09-MAY-2001.  
XX XX  
XX PF 03-NOV-2000; 2000EP-00309719.





QY 421 FHRGSAQSFLOTETSVI 438  
 DB 421 FHRASRAQSFLOTETSVI 438

## RESULT 15

ABP81992  
 ID ABP81992 standard; protein; 438 AA.

XX  
 AC ABP81992;

XX  
 DT 04-MAR-2003 (first entry)

XX  
 DE Human vasoactive intestinal polypeptide receptor 2 protein SEQ ID NO:471.

XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.

XX  
 OS Homo sapiens.

XX  
 PN WO200261087-A2.

XX  
 PD 08-AUG-2002.

XX  
 PF 19-DEC-2001; 2001WO-US050107.

XX  
 PR 19-DEC-2000; 2000US-0257144P.

XX  
 \*PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX  
 PI Burmer GC, Roush CL, Brown JP;

XX  
 DR WPI; 2003-046718/04.

XX  
 DR N-PSDB; AB242841.

XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.

XX  
 PS Disclosure; Fig 1; 523pp; English.

XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be

CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX  
 SQ Sequence 438 AA;

Query Match 99.4%; Score 2327; DB 6; Length 438;  
 Best Local Similarity 99.3%; Pred. No. 3.3e-225;  
 Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	MTLLPALLTCWLLAPVNSIHPECKFHLIEIQEETKCAELRSQTEKHKACSGWDNIT	60
DB	1	MTLLPALLTCWLLAPVNSIHPECKFHLIEIQEETKCTELLRSQTEKHKACSGWDNIT	60
QY	61	CWRPANVGTVTPCPKVPFSNFYSKAGNISKNCTSDGWSSETPPDFVDACGYDPEDESKI	120
DB	61	CWRPANVGTVTPCPKVPFSNFYSKAGNISKNCTSDGWSSETPPDFVDACGYDPEDESKI	120
QY	121	TFYILVKAIYTLGYSVLSMLATGSIILCLPRKLHCTRYIHNLFLSFILRAISVLVKD	180
DB	121	TFYILVKAIYTLGYSVLSMLATGSIILCLPRKLHCTRYIHNLFLSFILRAISVLVKD	180
QY	181	DVLYSSSGTLHCPDQPSNVGCKLSLVFLQYCI MANFFWLLVEGLYLETLLVAMLPFRRC	240
DB	181	DVLYSSSGTLHCPDQPSNVGCKLSLVFLQYCI MANFFWLLVEGLYLETLLVAMLPFRRC	240
QY	241	FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDTHDHSVPWVIRIPILISIIIVNVLFI	300
DB	241	FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDTHDHSVPWVIRIPILISIIIVNVLFI	300
QY	301	SIIRILLOKLTSPDVGGNDQSOYKELAKSTLLLIPLFGVHYMVFAVEPTISISSKYQILFE	360
DB	301	SIIRILLOKLTSPDVGGNDQSOYKELAKSTLLLIPLFGVHYMVFAVEPTISISSKYQILFE	360
QY	361	LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCRPTPSASRDYRVCGSFSHNGSEGAIQ	420
DB	361	LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCRPTPSASRDYRVCGSFSHNGSEGAIQ	420
QY	421	FHRGSAQSFLOTETSVI 438	
DB	421	FHRASRAQSFLOTETSVI 438	

Search completed: June 22, 2004, 08:57:33

Job time : 63 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 08:56:24 ; Search time 23 Seconds  
(without alignments)  
983.138 Million cell updates/sec

Title: US-09-983-000A-20  
Perfect score: 2342  
Sequence: 1 MRTLPPALITCWLAPVNS.....LQHRGSRAGSFLQTETSVI 438

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	2331	99.5	438	2	US-08-538-816A-1	Sequence 1, Appli
2	2331	99.5	438	2	US-09-076-651-1	Sequence 1, Appli
3	2331	99.5	438	4	US-09-208-394-1	Sequence 1, Appli
4	2239.5	95.6	431	2	US-08-538-816A-9	Sequence 9, Appli
5	2239.5	95.6	431	2	US-09-076-651-9	Sequence 9, Appli
6	2239.5	95.6	431	4	US-09-208-394-9	Sequence 9, Appli
7	2030	86.7	437	2	US-08-538-816A-2	Sequence 2, Appli
8	2030	86.7	437	2	US-09-076-651-2	Sequence 2, Appli
9	2030	86.7	437	4	US-09-208-394-2	Sequence 2, Appli
10	1153.5	49.3	467	2	US-08-811-897A-19	Sequence 19, Appl
11	1153.5	49.3	467	2	US-08-855-213-19	Sequence 19, Appl
12	1153.5	49.3	467	4	US-09-201-474-19	Sequence 19, Appl
13	1151.5	49.2	485	2	US-08-811-897A-17	Sequence 17, Appl
14	1151.5	49.2	485	2	US-08-855-213-17	Sequence 17, Appl
15	1151.5	49.2	485	4	US-09-201-474-17	Sequence 17, Appl
16	1150	49.1	525	2	US-08-811-897A-23	Sequence 23, Appl
17	1150	49.1	525	2	US-08-855-213-23	Sequence 23, Appl
18	1150	49.1	525	4	US-09-201-474-23	Sequence 23, Appl
19	1144.5	48.9	448	2	US-08-811-897A-22	Sequence 22, Appl
20	1144.5	48.9	448	2	US-08-855-213-22	Sequence 22, Appl
21	1144.5	48.9	448	4	US-09-201-474-22	Sequence 22, Appl
22	1143.5	48.8	448	2	US-08-811-897A-18	Sequence 18, Appl
23	1143.5	48.8	448	2	US-08-855-213-18	Sequence 18, Appl
24	1143.5	48.8	448	4	US-09-201-474-18	Sequence 18, Appl
25	1141.5	48.7	448	2	US-08-811-897A-16	Sequence 16, Appl
26	1141.5	48.7	448	2	US-08-855-213-16	Sequence 16, Appl
27	1141.5	48.7	448	4	US-09-201-474-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-538-816A-1  
; Sequence 1, Application US/08538816A  
; Patent No. 5831051  
; GENERAL INFORMATION:  
; APPLICANT: McJsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/538,816A  
; FILING DATE: 03-OCTOBER-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/437,466  
; FILING DATE: 09-MAY-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEFAX: 133521  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 438 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: Human PACAP/VIP R-2  
; HYPOTHEICAL: NO  
; US-08-538-816A-1

28 1129.5 48.2 495 2 US-08-811-897A-21 Sequence 21, Appl  
29 1129.5 48.2 495 2 US-08-855-213-21 Sequence 21, Appl  
30 1129.5 48.2 495 4 US-09-201-474-21 Sequence 21, Appl  
31 1127.5 48.1 513 2 US-08-811-897A-15 Sequence 15, Appl  
32 1127.5 48.1 513 2 US-08-855-213-15 Sequence 15, Appl  
33 1127.5 48.1 552 4 US-09-201-474-15 Sequence 15, Appl  
34 1126.5 48.1 552 2 US-08-811-897A-27 Sequence 27, Appl  
35 1126.5 48.1 552 2 US-08-855-213-27 Sequence 27, Appl  
36 1126.5 48.1 552 4 US-09-201-474-27 Sequence 27, Appl  
37 1126 48.1 553 2 US-08-811-897A-25 Sequence 25, Appl  
38 1126 48.1 553 2 US-08-855-213-25 Sequence 25, Appl  
39 1126 48.1 553 2 US-08-855-213-25 Sequence 25, Appl  
40 1126 48.1 553 4 US-09-201-474-25 Sequence 25, Appl  
41 1126 48.1 553 4 US-09-201-474-25 Sequence 25, Appl  
42 1126 48.1 553 4 US-09-201-474-25 Sequence 26, Appl  
43 1121 47.9 475 2 US-08-811-897A-26 Sequence 26, Appl  
44 1121 47.9 475 2 US-08-855-213-26 Sequence 26, Appl  
45 1121 47.9 475 4 US-09-201-474-26 Sequence 26, Appl

Query Match 99.5%; Score 2331; DB 2; Length 438;  
Best Local Similarity 99.5%; Pred. No. 8.6e-212;  
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60  
DB 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60  
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DB 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
QY 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRAIISVLVKD 180  
DB 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRAIISVLVKD 180  
QY 181 DVLVSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFLLVEGLYHLTLVAMLPERRC 240  
DB 181 DVLVSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFLLVEGLYHLTLVAMLPERRC 240  
QY 241 FLAYLLIGWGLPTVCIGANTAAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
DB 241 FLAYLLIGWGLPTVCIGANTAAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
QY 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSKYQILFE 360  
DB 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSKYQILFE 360  
QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCSSFSRNGSEGALQ 420  
DB 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCSSFSRNGSEGALQ 420  
QY 421 FHRGSAQSFLOTETSVI 438  
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 2  
US-09-076-651-1  
; Sequence 1, Application US/09076651  
; Patent No. 5882899  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/076,651  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/538,816  
; FILING DATE: 03-OCTOBER-1995  
; APPLICATION NUMBER: US 08/437,466  
; FILING DATE: 09-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Human PACAP/VIP R-2  
HYPOTHETICAL: NO  
US-09-076-651-1

Query Match 99.5%; Score 2331; DB 2; Length 438;  
Best Local Similarity 99.5%; Pred. No. 8.6e-212;  
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60  
DB 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60  
QY 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
DB 61 CWRPANVGETVTPCPKFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
QY 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRAIISVLVKD 180  
DB 121 TFYILVKAITYTLGYSVLSLATSIIILCLFRKLHCTRYIHNLFLSFLTRAIISVLVKD 180  
QY 181 DVLVSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFLLVEGLYHLTLVAMLPERRC 240  
DB 181 DVLVSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFLLVEGLYHLTLVAMLPERRC 240  
QY 241 FLAYLLIGWGLPTVCIGANTAAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
DB 241 FLAYLLIGWGLPTVCIGANTAAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
QY 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSKYQILFE 360  
DB 301 SIIRILLOKLTSPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPPISSKYQILFE 360  
QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCSSFSRNGSEGALQ 420  
DB 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCSSFSRNGSEGALQ 420  
QY 421 FHRGSAQSFLOTETSVI 438  
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 3  
US-09-208-394-1  
; Sequence 1, Application US/09208394  
; Patent No. 6316596  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/208,394  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/538,816  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Human PACAP/VIP R-2  
HYPOTHETICAL: NO  
US-09-208-394-1

Query Match 99.5%; Score 2331; DB 4; Length 438;  
Best Local Similarity 99.5%; Pred. No. 8.6e-212;  
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNIT 60

\*QY 61 CWRPANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120  
DB 61 CWRPANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKI 120

QY 121 TFYILVKAITYLGYSVLSMLATSGIILCLFRKLHCTRYNIHLNLFILRAISVLVKD 180  
DB 121 TFYILVKAITYLGYSVLSMLATSGIILCLFRKLHCTRYNIHLNLFILRAISVLVKD 180

QY 181 DVLVSSSTLHCPDQPSWVGCKLSLVFLQYCIIMANFVLLVEGLYHTLLVAMLPVPRRC 240  
DB 181 DVLVSSSTLHCPDQPSWVGCKLSLVFLQYCIIMANFVLLVEGLYHTLLVAMLPVPRRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNVLFI 300  
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNVLFI 300

QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
DB 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGLQ 420  
DB 361 LCLGSFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGLQ 420

QY 421 FHRGSAQSFLOTETSVI 438  
DB 421 FHRASRAQSFLOTETSVI 438

RESULT 4  
US-08-538-816A-9  
Sequence 9, Application US/08538816A  
Patent No. 5831051  
GENERAL INFORMATION:  
APPLICANT: Mojssov, Svetlana  
APPLICANT: Wei, Yang

TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/538,816A  
FILING DATE: 03-OCTOBER-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/437,466  
FILING DATE: 09-MAY-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Human PACAP/VIP R-2B  
HYPOTHETICAL: NO  
US-08-538-816A-9

Query Match 95.6%; Score 2239.5; DB 2; Length 431;  
Best Local Similarity 97.7%; Pred. No. 3.6e-203;  
Matches 424; Conservative 2; Mismatches 3; Indels 5; Gaps 2;

QY 5 LPPALLTCWLLAPVNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNITCWRP 64  
DB 3 LGPSL---YLL--VNSIHPECRFHELEIQEETKCAELLRSQTEKHKACSGVMDNITCWRP 57

QY 65 ANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKIIFYI 124  
DB 58 ANGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKIIFYI 117

QY 125 LVKAIYTLGYSVLSMLATSGIILCLFRKLHCTRYNIHLNLFILRAISVLVKDDVLY 184  
DB 118 LVKAIYTLGYSVLSMLATSGIILCLFRKLHCTRYNIHLNLFILRAISVLVKDDVLY 177

QY 185 SSSGTLHCPDQPSWVGCKLSLVFLQYCIIMANFVLLVEGLYHTLLVAMLPVPRRCFLAY 244  
DB 178 SSSGTLHCPDQPSWVGCKLSLVFLQYCIIMANFVLLVEGLYHTLLVAMLPVPRRCFLAY 237

QY 245 LLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNVLFIISIR 304  
DB 238 LLIGWGLPTVCIGAWTAARLYLEDTGCDTNDHSPVWVIRIPILISIVNVLFIISIR 297

QY 305 ILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFECLG 364  
DB 298 ILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFECLG 357

QY 365 SFQGLVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEGLQFHRG 424

Db 358 SFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSHNGSEGALQFHRA 417

QY 425 SRAQSFLOTETSVI 438

Db 418 SRAQSFLOTETSVI 431

## RESULT 5

US-09-076-651-9  
; Sequence 9, Application US/09076651  
; Patent No. 5882899  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/076,651  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/538,816  
; FILING DATE: 03-OCTOBER-1995  
; APPLICATION NUMBER: US 08/437,466  
; FILING DATE: 09-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 431 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: Human PACAP/VIP R-2B  
; HYPOTHETICAL: NO  
; US-09-076-651-9

Query Match 95.6%; Score 2239.5; DB 2; Length 431;  
Best Local Similarity 97.7%; Pred. No. 3.6e-203;  
Matches 424; Conservative 2; Mismatches 3; Indels 5; Gaps 2;  
QY 5 LPPALLTCWLLAPVNSIHPECRFHLIEQEEETKCAELLRSQTEKHKACSGVWDNITCWRP 64  
Db 3 LGPSL---YLL--VNSIHPECRFHLIEQEEETKCAELLRSQTEKHKACSGVWDNITCWRP 57  
QY 65 ANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKITFYI 124  
Db 58 ANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPDESKITFYI 117  
QY 125 LVKAIYTTGYSVLSMLATGSIILCLFRKLHCTRYIHLNLFSLFRLAISVLVKDDVLY 184  
Db 118 LVKAIYTTGYSVLSMLATGSIILCLFRKLHCTRYIHLNLFSLFRLAISVLVKDDVLY 177

QY 185 SSSGTLHCPDQSSWVGCKLSLVELOYCIMANFFWLLVEGLYLTLLVAMLPDRCFLAY 244  
Db 178 SSSGTLHCPDQSSWVGCKLSLVELOYCIMANFFWLLVEGLYLTLLVAMLPDRCFLAY 237  
QY 245 LLIGWGLPTVCIGAWTAARLYLEDTGWDTHDHSVPMWVIRIPILISIIIVNVLFIISIR 304  
Db 238 LLIGWGLPTVCIGAWTAARLYLEDTGWDTHDHSVPMWVIRIPILISIIIVNVLFIISIR 297  
QY 305 ILLQKLTSPDVGNDOSQYKRLAKSTLLIPLFGVHYMVEAFVPISSISKYQILFELCLG 364  
Db 238 ILLQKLTSPDVGNDOSQYKRLAKSTLLIPLFGVHYMVEAFVPISSISKYQILFELCLG 357  
QY 365 SFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSHNGSEGALQFHRA 424  
Db 358 SFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSHNGSEGALQFHRA 417  
QY 425 SRAQSFLOTETSVI 438  
Db 418 SRAQSFLOTETSVI 431

## RESULT 6

US-09-208-394-9  
; Sequence 9, Application US/09208394  
; Patent No. 6316596  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,394  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/538,816  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 431 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: Human PACAP/VIP R-2B  
; HYPOTHETICAL: NO  
; US-09-208-394-9

Query Match 95.6%; Score 2239.5; DB 4; Length 431;



Best Local Similarity 97.7%; Pred. No. 3.6e-203;  
Matches 424; Conservative 2; Mismatches 3; Indels 5; Gaps 2;  
QY 5 LPPALLTCLLAPVNSIHPECRFHLEIOEETKCAELLRSQTEKHKACSGWNDNITCWRP 64  
DB 3 LGPSL---YLL--VNSIHPECRFHLEIOEETKCAELLRSQTEKHKACSGWNDNITCWRP 57  
QY 65 ANVGETVTPCKVFNFSYKAGNISKNCTSDGSETPPDFVDACGYSDPEDESKITFYI 124  
DB 58 ANVGETVTPCKVFNFSYKAGNISKNCTSDGSETPPDFVDACGYSDPEDESKITFYI 117  
QY 125 LVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLRAISVLVXDDVLY 184  
DB 118 LVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLRAISVLVXDDVLY 177  
QY 185 SSGTTLHCPDQSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP RRCFLAY 244  
DB 178 SSGTTLHCPDQSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP RRCFLAY 237  
QY 245 LLIGMLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLSIIR 304  
DB 238 LLIGMLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLSIIR 297  
QY 305 ILLQKLTSPDVGNQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIG 364  
DB 298 ILLQKLTSPDVGNQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIG 357  
QY 365 SFGGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLAQFHG 424  
DB 358 SFGGLVAVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLAQFHG 417  
QY 425 SRAQSFLOTETSVI 438  
DB 418 SRAQSFLOTETSVI 431

RESULT 7  
US-08-538-816A-2  
; Sequence 2, Application US/08538816A  
; Patent No. 5831051  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/538,816A  
; FILING DATE: 03-OCTOBER-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/437,466  
; FILING DATE: 09-MAY-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684  
TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: RPACAP-3/RVIP-2  
; HYPOTHETICAL: NO  
; US-08-538-816A-2

Query Match 86.7%; Score 2030; DB 2; Length 437;  
Best Local Similarity 87.4%; Pred. No. 2.2e-183;  
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;  
QY 12 CWLLAPVNSIHPECRFHLEIOEETKCAELLRSQTEKHKACSGWNDNITCWRPANVGTV 71  
DB 11 CWLLVRVSSIHPECRFHLEIOEETKCAELLSSQTEHQACSGWNDNITCWRPADVGTV 70  
QY 72 TVPCPKVFNFSYKAGNISKNCTSDGSETPPDFVDACGYSDPEDESKITFYILKAIYT 131  
DB 71 TVPCPKVFNFSYKAGNISKNCTSDGSETPPDFVDACGYNDPEDESKISFYILKAIYT 130  
QY 132 LGYSVLSMLATGSIILCLFRKLHCTRNVIHLNLFSLRAISVLVXDDVLYSSGTLH 191  
DB 131 LGYSVLSMLTGTGSIILCLFRKLHCTRNVIHLNLFSLRAISVLVXDDVLYSSGTLR 190  
QY 192 CPDQSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLP RRCFLAYLLHGMGL 251  
DB 191 CHDQASWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAILPPSRCLAYLLHGMGI 250  
QY 252 PTVCGIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISITVNFVLSIIRILLOKLT 311  
DB 251 PSVCIGAWTATRLSLEDTCGWDNDHSPVWVIRIPILISITVNFVLSIIRILLOKLT 310  
QY 312 SPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISISKYQILFELCIGSFQGLV 371  
DB 311 SPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVFPISIGISTYQILFELCVGSFQGLV 370  
QY 372 AVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLAQFHGSRQAQSF 431  
DB 371 AVLYCFLNSEVOCELKRWRCPTPSASRDYRVCGSSFRNGSEGLAQFHGSRQAQSF 430  
QY 432 QTETSVI 438  
DB 431 QSETSVI 437

RESULT 8  
US-09-076-651-2  
; Sequence 2, Application US/09076651  
; Patent No. 5882899  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED  
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/538,816A  
; FILING DATE: 03-OCTOBER-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/437,466  
; FILING DATE: 09-MAY-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/076,651  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/538,816  
; FILING DATE: 03-OCTOBER-1995  
; APPLICATION NUMBER: US 08/437,466  
; FILING DATE: 09-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: RPACAP-3/RVIP-2  
; HYPOTHETICAL: NO  
; US-09-076-651-2

Query Match 86.7%; Score 2030; DB 2; Length 437;  
Best Local Similarity 87.4%; Pred. No. 2.2e-183;  
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY	12	CWLLAPVNSHPHPCRFHLEIQEETKCAELLRSQTEKHKACSGVWDNITCWRPANVGETV	71
DB	11	CWLLVRVSSHPCRFHLEIQEETKCAELLSSQTEKHKACSGVWDNITCWRPADVGETV	70
QY	72	TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKITFYILVKAITY	131
DB	71	TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPEDESKISFYILVKAITY	130
QY	132	LGYSVLSMISATGSIICLFRKLHCTRNTHNLFLSFILRAISVLVKDVLVSSSGTLH	191
DB	131	LGYSVLSMISLTTGSIICLFRKLHCTRNTHNLFLSFMLRAISVLVKDVLVSSSGLLR	190
QY	192	CPDOPSSWVGCKSLVFLQYCIMANFVLLVEGLYHLTLVAMLPFRRCFLAYLLIGWL	251
DB	191	CHDOPASWVGCKSLVFFQYCIMANFVLLVEGLYHLTLVAILPPSRCFLAYLLIGWI	250
QY	252	PTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLFISIRILLQKLT	311
DB	251	PSVCIGAWTATRLSLEDTCGWDNDHSPVWVIRMPILISIVNFALFISIRILLQKLT	310
QY	312	SPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFELCLGSFQGLV	371
DB	311	SPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAAFPIGISTYQILFELCVGSFQGLV	370
QY	372	AVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCSSFRNGSEGALQFHRGSRQSF	431
DB	371	AVLYCFNLSEVQCELRKWRGLCLTQAGSRDYLHWSMSRNGESALQIHRGSRQSF	430
QY	432	QTSVSI 438	
DB	431	QTSVSI 437	

## RESULT 9

US-09-208-394-2  
; Sequence 2, Application US/09208394  
; Patent No. 6316596  
; GENERAL INFORMATION:  
; APPLICANT: Mojsov, Svetlana  
; APPLICANT: Wei, Yang  
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED

; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,394  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/538,816  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: RPACAP-3/RVIP-2  
; HYPOTHETICAL: NO  
; US-09-208-394-2

Query Match 86.7%; Score 2030; DB 4; Length 437;  
Best Local Similarity 87.4%; Pred. No. 2.2e-183;  
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY	12	CWLLAPVNSHPHPCRFHLEIQEETKCAELLRSQTEKHKACSGVWDNITCWRPANVGETV	71
DB	11	CWLLVRVSSHPCRFHLEIQEETKCAELLSSQTEKHKACSGVWDNITCWRPADVGETV	70
QY	72	TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDESKITFYILVKAITY	131
DB	71	TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPEDESKISFYILVKAITY	130
QY	132	LGYSVLSMISATGSIICLFRKLHCTRNTHNLFLSFILRAISVLVKDVLVSSSGTLH	191
DB	131	LGYSVLSMISLTTGSIICLFRKLHCTRNTHNLFLSFMLRAISVLVKDVLVSSSGLLR	190
QY	192	CPDOPSSWVGCKSLVFLQYCIMANFVLLVEGLYHLTLVAMLPFRRCFLAYLLIGWL	251
DB	191	CHDOPASWVGCKSLVFFQYCIMANFVLLVEGLYHLTLVAILPPSRCFLAYLLIGWI	250
QY	252	PTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLFISIRILLQKLT	311
DB	251	PSVCIGAWTATRLSLEDTCGWDNDHSPVWVIRMPILISIVNFALFISIRILLQKLT	310
QY	312	SPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFELCLGSFQGLV	371
DB	311	SPDVGGNDOSQYKRLAKSTLLIPLFGVHYMVFAAFPIGISTYQILFELCVGSFQGLV	370
QY	372	AVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCSSFRNGSEGALQFHRGSRQSF	431
DB	371	AVLYCFNLSEVQCELRKWRGLCLTQAGSRDYLHWSMSRNGESALQIHRGSRQSF	430



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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-855-213-19

Query Match          49.3%; Score 1153.5; DB 2; Length 467;
Best Local Similarity 49.7%; Pred. No. 1.3e-100;
Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCWLLAPVNSIHPECRFHLEIQEBETKCAEL-----LRSQTEKHKACSGVWNDITCWR 63
Db 9 LTALLPVAIAMHSDCIF---KKEQAMCLERIORANDLMGLNESPSPGCPGMWMDNITCWK 64
QY 64 PANVGETVTVPCKVGSNF-----YSKAGNISKNCTSDGWS 100
Db 65 PAQGEWLVSCPEVFRIFPDQVMTETIGDSGFADSNLSLEITDMGVVGRNCTEDGWS 124
QY 101 TPDFVDACGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
Db 125 PFPHYFACGFDDEPESGDQDYVYLSVKALYTVGYSTSLATLTAMVILCRFRKLHCTR 184
QY 159 NYIHLNLFILRAISLVKDDVLYSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFF 218
Db 185 NFTHMNLVFSFMLRAISLVKIDVLYAEQDSSHC---FVSTVECKAVMVFFHYCVVSNYF 241
QY 219 WLLVEGLYLHLLV-AMLPERRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDH 277
Db 242 WLFIEGLYLLTLLVETFPERRFYWYTIIGWGTPTVCVTVVAVLRLYFDGACGWDNDS 301
QY 278 SVPMWVIRIPILISITVNFVLFISIRILLOKUTSPDVGNDSQYKRLAKSTLLIPLF 337
Db 302 TALWVWIKGVPVGSIMVNFVLFIGIILVQKQSPDMGNGESSIYLRLARSTLLIPLF 361
QY 338 GVHYMFAVFPISISSKYQILFELCLGSPQGLVAVLYCFLNSEVQCELKRWRSRCP 397
Db 362 GIHTVFAFSPENVKRERLVFELGLGSPQGVVAVLYCFLNGEVOAETKRKRWSKVN 421
QY 398 SASRDYRVCSSFRNRSSEGLQFHRGSRQAQSFQ 432
Db 422 YFTMDFKHRHPSLASSGVNGTQLSLSSSSQLR 456

RESULT 12
US-09-201-474-19
; Sequence 19, Application US/09201474
; Patent No. 639316
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 63991610
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/201,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,897
; FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-201-474-19

Query Match          49.3%; Score 1153.5; DB 4; Length 467;
Best Local Similarity 49.7%; Pred. No. 1.3e-100;
Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCWLLAPVNSIHPECRFHLEIQEBETKCAEL-----LRSQTEKHKACSGVWNDITCWR 63
Db 9 LTALLPVAIAMHSDCIF---KKEQAMCLERIORANDLMGLNESPSPGCPGMWMDNITCWK 64
QY 64 PANVGETVTVPCKVGSNF-----YSKAGNISKNCTSDGWS 100
Db 65 PAQGEWLVSCPEVFRIFPDQVMTETIGDSGFADSNLSLEITDMGVVGRNCTEDGWS 124
QY 101 TPDFVDACGYSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158
Db 125 PFPHYFACGFDDEPESGDQDYVYLSVKALYTVGYSTSLATLTAMVILCRFRKLHCTR 184
QY 159 NYIHLNLFILRAISLVKDDVLYSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFF 218
Db 185 NFTHMNLVFSFMLRAISLVKIDVLYAEQDSSHC---FVSTVECKAVMVFFHYCVVSNYF 241
QY 219 WLLVEGLYLHLLV-AMLPERRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDH 277
Db 242 WLFIEGLYLLTLLVETFPERRFYWYTIIGWGTPTVCVTVVAVLRLYFDGACGWDNDS 301
QY 278 SVPMWVIRIPILISITVNFVLFISIRILLOKUTSPDVGNDSQYKRLAKSTLLIPLF 337
Db 302 TALWVWIKGVPVGSIMVNFVLFIGIILVQKQSPDMGNGESSIYLRLARSTLLIPLF 361
QY 338 GVHYMFAVFPISISSKYQILFELCLGSPQGLVAVLYCFLNSEVQCELKRWRSRCP 397
Db 362 GIHTVFAFSPENVKRERLVFELGLGSPQGVVAVLYCFLNGEVOAETKRKRWSKVN 421
QY 398 SASRDYRVCSSFRNRSSEGLQFHRGSRQAQSFQ 432
Db 422 YFTMDFKHRHPSLASSGVNGTQLSLSSSSQLR 456

RESULT 13
US-08-811-897A-17
; Sequence 17, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 585878710

```

TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING  
TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESS: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,897A  
FILING DATE: 05-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,986  
FILING DATE: February 25, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, David S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 44168-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-811-897A-17

Query Match 49.2%; Score 1151.5; DB 2; Length 485;  
Best Local Similarity 48.6%; Pred. No. 2.2e-100;  
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;  
QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLTEIQTETKCAEL-----LRSQTEKHKACSG 54  
DB 18 MASIAQVSLAALLLPMATAMHSDCIF----KKEQAMCLEKIQRVNDLMLGNDSSPGCPG 73  
QY 55 VWDNITCWRPANVGETTVPCPKVFSNF-----YSKAGNISK 91  
DB 74 MWDNITCWRPANVGETTVPCPKVFSNF-----YSKAGNISK 91  
QY 92 NCTSDGSETFPDFVDACGYSDPEDES--KITFYLVKAIYTLGYSVLSMLSLATGSIILC 149  
DB 134 NCTEDGSEFPFPHYFDACGFEYESETGDQDYVYLVKALVTGVSTSLVTLTTAMWILC 193  
QY 150 LFRKLHCTRYNIHLNLFILRAISVLVKDDVLYSSSGTILHCPDQPSWVGCKLSVLFL 209  
DB 194 RFRKLHCTRYNIHLNLFILRAISVLVKDDVLYSSSGTILHCPDQPSWVGCKLSVLFL 209  
QY 210 QYICMANPFWLLVEGLYHLTLV-AMLPKRCFLAYLLIGLPTVCIGAMTAARLYLED 268  
DB 251 HCVVSNVFWLFIKGLYHLTLVETFFPERFYFYIIGHTPTVCVSWAMRLYLED 310  
QY 269 TGCWDTNDSVWVWIRIPILISIVNLFVLSIRILLOKLTSPDVGNDQSQYKRLAK 328  
DB 311 TGCWDMNDNTALWVIKGPVGSIMVNFVLIIGIIVLVKQLQSDMGNESSIYLRAR 370  
QY 329 STLLLLPLFGVHYVYAFVPIISISKYQILLCGLSGQGLVAVLYCFINSEVQCELR 388  
DB 371 STLLLLPLFGVHYVYAFVPIISISKYQILLCGLSGQGLVAVLYCFINSEVQCELR 388  
QY 389 KWRSCRPTSPSARDYRVCGSSFSRNGSGALQFHRGSAQS 429  
DB 431 KWRSKVNYRYTMDKXHPHSLASSGVNGGTQLSILSKSS 471

RESULT 14  
US-08-855-213-17  
Sequence 17, Application US/08855213  
Patent No. 5892004  
GENERAL INFORMATION:  
APPLICANT: ONDA, Haruo  
APPLICANT: OHTAKI, Tetsuya  
APPLICANT: MASUDA, Yasushi  
APPLICANT: KITADA, Chieko  
APPLICANT: ISHIBASHI, Yoshihiro  
APPLICANT: HOSoya, Masaki  
APPLICANT: OGI, Kazuhiro  
APPLICANT: MIYAMOTO, Yasunori  
APPLICANT: HABATA, Yugo  
APPLICANT: SHIMAMOTO, No. 5892004io  
TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR  
TITLE OF INVENTION: PREPARING SAID PROTEIN, AND USE THEREOF  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESS: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/855,213  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,986  
FILING DATE: 25-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, David S.  
REGISTRATION NUMBER: 34235  
REFERENCE/DOCKET NUMBER: 44168  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-855-213-17

Query Match 49.2%; Score 1151.5; DB 2; Length 485;  
Best Local Similarity 48.6%; Pred. No. 2.2e-100;  
Matches 224; Conservative 72; Mismatches 126; Indels 39; Gaps 6;  
QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLTEIQTETKCAEL-----LRSQTEKHKACSG 54  
DB 18 MASIAQVSLAALLLPMATAMHSDCIF----KKEQAMCLEKIQRVNDLMLGNDSSPGCPG 73  
QY 55 VWDNITCWRPANVGETTVPCPKVFSNF-----YSKAGNISK 91  
DB 74 MWDNITCWRPANVGETTVPCPKVFSNF-----YSKAGNISK 91  
QY 92 NCTSDGSETFPDFVDACGYSDPEDES--KITFYLVKAIYTLGYSVLSMLSLATGSIILC 149  
DB 134 NCTEDGSEFPFPHYFDACGFEYESETGDQDYVYLVKALVTGVSTSLVTLTTAMWILC 193  
QY 150 LFRKLHCTRYNIHLNLFILRAISVLVKDDVLYSSSGTILHCPDQPSWVGCKLSVLFL 209

194 RFRKLCSTRNFIHNLVFSFMLRAISVFIKOWILYAEQDSNHC---FVSTVECKAVMVFF 250

210 QYCI MANFPWLLVEGLYHTLLV-AMLP PRCFLAYLLIGWLPVCIGANTAA RLYLLED 268

251 HCVVSNYFWLFIEGLYHTLLVETFPFERRFYFYWIIIGWTPFCVSVWAMLELYFDD 310

269 TGCWDTNDHSVPWVIRIPILISITIVNVLFSIIRILLQKLTSPDVGNDQSOYKRLAK 328

311 TGCWDMNDTALWVVIKPPVGVSGMWNVFLFIIIVILVQKLSQSPDMGNGNSSIVLRAR 370

329 STLLIPLFGVHYMVFAVPFPISSKYOILFELCLGSPQGLVAVLYQFLNSEVQCELR 388

371 STLLIPLFGIHVTVFAFSPENVSCKRBLVFEJGLGSPQGFVAVLYCFNLGEVQAEIKR 430

389 KWRRCPTPSASRDYRVCGSSFSRNGSEGALQFHRGSAQS 429

431 KWRSKVKNRYFTMDFKRRHPSLASSGVNNGTQLSLTSSSS 471

RESULT 15

US-09-201-474-17

; Sequence 17, Application US/09201474

; Patent No. 6399316

; GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: MASUDA, Yasushi

; APPLICANT: KITADA, Chieko

; APPLICANT: ISHIBASHI, Yoshihiro

; APPLICANT: HOSOYA, Masaki

; APPLICANT: OGI, Kazuhiro

; APPLICANT: MIYAMOTO, Yasunori

; APPLICANT: HABATA, Yugo

; APPLICANT: SHIMAMOTO, No. 6399316io

; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING

; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BROWNSTEIN, ROBERTS &

[illegible]

Search completed: June 22, 2004, 09:00:09  
Job time : 25 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:54:08 ; Search time 45 Seconds  
(without alignments)  
3071.044 Million cell updates/sec

Title: US-09-983-000a-20  
Perfect score: 2342  
Sequence: 1 MRTLPPALLTCWLLAPVNS.....LQFHGRSRAQSFLETSTVI 438

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_plant.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1324	56.5	426	13 Q802T6	Q802t6 fugu rubrip
2	1151	49.1	459	11 Q8BGA4	Q8bga4 mus musculus
3	1141.5	48.7	444	13 Q9VHC6	Q9vhc6 rana ridibu
4	1126	48.1	496	11 Q8BLT3	Q8blt3 mus musculus
5	1124	48.0	465	13 Q9PTK1	Q9ptk1 xenopus lae
6	1114.5	47.6	455	13 Q90Y10	Q90y10 rana ridibu
7	1100	47.0	418	13 Q91BG2	Q91bg2 gallus gall
8	1099	46.9	434	13 Q802T7	Q802t7 fugu rubrip
9	1092	46.6	480	13 Q90Y07	Q90y07 rana ridibu
10	1090	46.5	465	13 Q73769	Q73769 carassius a
11	1084.5	46.3	495	13 Q90Y08	Q90y08 rana ridibu
12	1059	45.2	419	13 Q8AXV3	Q8axv3 fugu rubrip
13	1056.5	45.1	465	13 Q90Y09	Q90y09 rana ridibu
14	1041	44.4	419	13 Q8AXV4	Q8axv4 fugu rubrip
15	1020.5	43.6	374	6 Q8WMR0	Q8wmr0 ovis aries
16	1003.5	42.8	528	4 Q81V17	Q81v17 homo sapien

17	996.5	42.5	402	6 Q8WMO9	Q8wmq9 ovis aries
18	971.5	41.5	438	13 Q73768	Q73768 carassius a
19	939	40.1	438	13 Q8AXV2	Q8axv2 fugu rubrip
20	876	37.4	423	6 Q9N1F8	Q9n1f8 bos taurus
21	872	37.2	439	11 Q9WU99	Q9wu99 rattus norv
22	872	37.2	441	6 Q9TUJ0	Q9tuj0 bos taurus
23	870	37.1	423	6 Q9BDH9	Q9bdh9 bos taurus
24	846.5	36.1	404	6 Q9TUJ1	Q9tuj1 bos taurus
25	844.5	36.1	407	6 Q9BDI0	Q9bdi0 ovis aries
26	764	32.6	595	6 Q9TU31	Q9tu31 canis famli
27	760.5	32.5	542	13 Q9PVD2	Q9pvd2 brachydanio
28	756.5	32.3	591	11 Q91WV4	Q91wv4 mus musculu
29	754.5	32.2	589	6 Q7YR13	Q7yri3 cervus elap
30	754.5	32.2	591	11 Q80WU8	Q80wu8 mus musculu
31	747	31.9	536	13 Q9PVD3	Q9pvd3 brachydanio
32	723.5	30.9	359	4 Q9HB45	Q9hb45 homo sapien
33	707	30.2	621	4 Q8N429	Q8n429 homo sapien
34	688	29.4	575	13 Q9PWB7	Q9pwb7 brachydanio
35	684.5	29.2	546	11 Q91V95	Q91v95 mus musculu
36	681.5	29.1	490	13 Q8UVY5	Q8uvy5 xenopus lae
37	681.5	29.1	492	13 Q9PUK1	Q9puk1 hoplobatrac
38	673	28.7	489	13 Q8UVY4	Q8uvy4 rana pipien
39	668.5	28.5	455	4 Q86X15	Q86x15 homo sapien
40	652.5	27.9	512	11 Q80YAI	Q80yal mus musculu
41	648	27.7	485	11 Q8K0B5	Q8k0b5 mus musculu
42	622.5	26.6	409	4 Q86YG9	Q86yg9 homo sapien
43	509	21.7	168	13 Q9YHC7	Q9yhc7 rana ridibu
44	501	21.4	445	13 Q98UC2	Q98uc2 ameivurus ne
45	495	21.1	437	6 Q8WML8	Q8wml8 tupaiia bela

## ALIGNMENTS

## RESULT 1

Q802T6	Q802T6	PRELIMINARY;	PRT;	426 AA.
ID	Q802T6			
AC	Q802T6			
DT	01-JUN-2003 (TREMREL. 24, Created)			
DT	01-JUN-2003 (TREMREL. 24, Last sequence update)			
DT	01-OCT-2003 (TREMREL. 25, Last annotation update)			
DE	Vasoactive intestinal peptide receptor.			
GN	VIPR2B.			
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC	Tetraodontidae; Tetraodontidae; Takifugu.			
OX	NCBI_TaxID=31033;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Cardoso J.C.R., Power D.M., Elgar G., Clark M.S., Canario A.V.M.;			
RT	"Isolation and characterisation of the secretin receptor family			
RT	members in Fugu rubripes."			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ408878; CAC83861.1;			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0004930; F:G-protein coupled receptor activity; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	InterPro; IPR000832; GPCR_secretin.			
DR	InterPro; IPR001879; hormn_receptor.			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	Pfam; PF02793; HRM; 1.			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	SMART; SM00008; HormR; 1.			
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.			
DR	PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.			
DR	Receptor.			
SK	SEQUENCE 426 AA; 48447 MW; 9D8C4AAF8407E92A CRC64;			

Query Match 56.5%; Score 1324; DB 13; Length 426;  
Best Local Similarity 58.8%; Pred. No. 2.5e-112;  
Matches 245; Conservative 62; Mismatches 104; Indels 6; Gaps 3;





Query Match 48.7%; Score 1141.5; DB 13; Length 444;  
 Best Local Similarity 51.9%; Pred. No. 1.1e-95;  
 Matches 233; Conservative 65; Mismatches 128; Indels 23; Gaps 10;

QY 5 LPALLTCLWLLAPVNSIIPEC--RHLLEIQEETKCAELLRSQTEKKKACSGVNDNITCW 62  
 DB 4 LPALLTCLWLLAPVNSIIPEC--RHLLEIQEETKCAELLRSQTEKKKACSGVNDNITCW 60

QY 63 RPANGETVTPCPKVFNSFYKA--GNISKNCTSDGMSVTPP--DFVACGYS--DPDEDE 117  
 DB 61 PSASIGEVVLLQCPGYFSNFTTGTGTVNGVSKNCTSEGMSVMPATYAAACGFSNDTPTPE 120

QY 118 SKITYIILVKAITYTILGYSVLSMSLATGSIILCLFKLHCTRYIHLNLFSLRAISVL 177  
 DB 121 QQTVPFGAIGTKYTIGHSLSLSLSLAAMIIICIFLKLHCTRYIHLNLFSLRAISVL 180

QY 178 VKDDVLYSSSGTLHCPDQPSWVGCKLSLVFQYCYCIMANFFVLLVEGLYHLTLV--AMLP 236  
 DB 181 IKDIVLFSGESDHC---HVGSGVCKAAMVFQYCYCIMANFFVLLVEGLYHLTLV--SFP 237

QY 237 PRRCFLAYLLIGWGLPTVCIQAWTAARLYLEDTGWDNDHVSVPWVIRIPILISILVNF 296  
 DB 238 EKKYFWWYIILGWGAPSVFITANSLARVYFDTGWDNTHESH--WIIKTPILVLSILVNF 296

QY 297 VLFISIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVEPISISSKYQ 356  
 DB 297 ILFICIRILVOKLHSPDVGNDQSQYKRLAKSTLLIPLFGVHYVMVFAVEPISISSKYQ 356

QY 357 ILFELCLGSGFQGLVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSE 416  
 DB 357 LVFELLILGSGFQGLVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSE 416

QY 417 GALQFH-----RGSRAOSFIQTETSVI 438  
 DB 417 FSTQISMLTKCSPKTRCSCSF-QAEFSLV 444

RESULT 4  
 Q9BLT3 PRELIMINARY; PRT; 496 AA.

AC Q9BLT3  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pituitary adenylate cyclase activating polypeptide type I receptor precursor.  
 GN ADCYAP1R1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK042820; BAC31372.1; -  
 DR PIR; PT0546; PT0698.  
 DR MGD; MGI:108449; Adcyap1r1.  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.  
 DR InterPro; IPR000832; GPCR\_secretin.  
 DR InterPro; IPR001879; hormn\_receptor.  
 DR Pfam; PF00002; 7tm\_2; 1.  
 DR Pfam; PF02793; HRM\_1.  
 DR PRINTS; PR00249; GPCRSECRETIN.  
 DR SMART; SM00008; Hormr; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.

DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS02027; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS02661; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 SQ SEQUENCE 496 AA; 56649 MW; D6C6446F1E086939 CRC64;

Query Match 48.1%; Score 1126; DB 11; Length 496;  
 Best Local Similarity 46.5%; Pred. No. 3.4e-94;  
 Matches 225; Conservative 66; Mismatches 125; Indels 68; Gaps 8;

QY 10 LTCWLLAPVNSIIPEC--RHLLEIQEETKCAEL-----LRSQTEKKKACSGVNDNITCW 62  
 DB 9 LTALLLPMALAMHSDCIF---KKEQAWCLERIORANDLMGLNLSPPCPGMWNDNITCW 64

QY 63 RPANGETVTPCPKVFNSNF-----YSKAGNISKNCTSDGMS 99  
 DB 65 KPAQIGEMVLYSCPEVFRIFNPDPQVMTTETGDSGFADSNLSLEITDMGVVGRNCTEDGMS 124

QY 100 ETFFPDVDCGYSD--PEDESKITFYIILVKAITYTILGYSVLSMSLATGSIILCLFKLHCT 157  
 DB 125 EFPFHYFDACGFDYEPESGDQDYVLYSVKALYTVGYSTPLVTLTAMVILCRFKLHCT 184

QY 158 RNYIHLNLFSLRAISVLKDDVLYSSSGTLHCPDQPSWVGCKLSLVFQYCYCIMANF 217  
 DB 185 RNFIHNLVFSVPMRAISVFIKDWILYAEQSSHC---FVSTVECKAVNVFHYCVVSNY 241

QY 218 FVLLVEGLYHLTLV--AMLP--PRRCFLAYLLIGWGLPTVCIQAWTAARLYLEDTGWDND 276  
 DB 242 FVLLVEGLYHLTLV--AMLP--PRRCFLAYLLIGWGLPTVCIQAWTAARLYLEDTGWDND 301

QY 277 HSPVWVIRIPILISILVNFVIFISIRILLOKLTSPDVGNDQSQY----- 323  
 DB 302 STALWVWIKVPGVVGSTMVNFVIFIGIIILLVQKQSPDMGNGNESSYFSCVKYCKPQR 361

QY 324 -----KRLAKSTLLIPLFGVHYVMVFAVEPISISSKYQILFELCLGSGFQ 368  
 DB 362 AQCHSKMSELSITILRLARSTLLIPLFGIHYTVFAFSPENVKRERLVFELGSGFQ 421

QY 369 LVVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEALQPHRGSRAQ 428  
 DB 422 FVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVCGSFSRNGSEALQPHRGSRAQ 481

QY 429 SFIQ 432  
 DB 482 SOLR 485

RESULT 5  
 Q9PTK1 PRELIMINARY; PRT; 465 AA.

AC Q9PTK1  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Pituitary adenylate cyclase-activating polypeptide type I receptor.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20419093; PubMed=10965909;  
 RA Hu Z., Lelievre V., Tam J., Cheng J.W., Fuenzalida G., Zhou X.,  
 RA Maschek J.A.;  
 RT "Molecular cloning of growth hormone-releasing hormone/pituitary  
 RT adenylate cyclase-activating polypeptide in the frog Xenopus laevis:  
 RT brain distribution and regulation after castration.";  
 RL Endocrinology 141:3366-3376(2000).  
 DR EMBL; AF187878; AAF16939.1; -  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.

DR	GO; GO:0004930; F,G-protein coupled receptor activity; IEA.
DR	GO; GO:0004872; Fireceptor activity; IEA.
DR	InterPro; IPR000832; GPCR secretin.
DR	InterPro; IPR001879; hormn_receptor.
DR	Pfam; PF00002; 7tm_2; 1.
DR	Pfam; PF02793; HRM; 1.
DR	PRINTS; PR00249; GPCRSECRETIN.
DR	SMART; SM00008; Hormr; 1.
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR	PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW	Receptor.
SQ	SEQUENCE 455 AA; 52411 MW; 8894D68D4810B2C1 CRC64;
	Query Match 47.6%; Score 1114.5; DB 13; Length 455;
	Best Local Similarity 48.9%; Pred.No.3.4e-93;
	Matches 219; Conservative 72; Mismatches 120; Indels 37; Gaps 9
QY	9 LLTCWLLAPVNS-----IHPCEFRHLEIQEETKCAEL----LRSQTEKHKACSGWDN 58
DB	4 LRLRYLLLIWASSLMAVMHYPC-----VIKKEETCLEKI QKLELEMWDSMPGCGMDN 59
QY	59 ITCWRRPANVGCTVTVPCKVFS-----NFYSK-----AGNISKNCTSDGMSETFPPDFV 106
DB	60 ITCMWPAVGVKVAIRCPANFMSIDSEDGMDFDYDRESHLEGVISRNCTENGWSDDPHYS 119
QY	107 DACGY-----SDPEDESKITFYILKYATLYIGYSVLSMLATGSII LCFLRKLHCTRNVIH 162
DB	120 DACCDFDNETGPDDQ--TVPLSVKALYTGVYSTSLVATTAMVILCFRKLHCTRNFIH 176
QY	163 LNLFSLSELRAISVLVKDDLVLYSSSGTLHCPODPSSWGCKSLVFLCYCI MANEFWLIV 222
DB	177 MNLFVSFTLRAISVFIDEVLVAEQDSNHC---HVSTVECKAVMVFFHYCVMSNTFWLFI 233
QY	223 EGLYLHTLLV-AMLFP RRCLFAYLLI GWGLTPVCIGAWTAARLYLEDTGCDTNDHSVPM 281
DB	234 EGLYLTLLVETFPERRYFYWTIIGWGTPLICVTIWA VLRHLHPDQGCWEMNNVALV 293
QY	282 WVRIPILISLVNVFLFISIRILLOKLTSPDVGDNDQSQVKRIAKSTLLILLPLFGVHY 341
DB	294 WVIKGPVIASIMINFLPVFGIIIILVQKLPDIDGNESSIYLRARS TLLIPLIFGIHY 353
QY	342 MVFAVFPVISISKYQLFELFCIGSGFGLVWVLYFLNSEQVCELRKWRSCRPTPSASR 401
DB	354 TVFAFSPENVSKRELVPFELGLGSPQGFFVAILCYFLNGEVQSEIKRKWRSMKVNRYPFV 413
QY	402 DYRVCGSFSRNGSEGALQFHRSQAQS 429
DB	414 DFKEHRHPSLAGSVNGGTQLSILSKSS 441

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RESULT 7
Q91BG2          PRELIMINARY;   PRT;   418 AA.
ID
AC Q91BG2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Vasoactive intestinal peptide receptor (Fragment).
GN CV1PR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21218647; PubMed=11319166;
RA Katsaku N., Shimada K., Ohkubo T., Saito N., Suzuki T., Matsuda Y.,
RA zadworny D.;
RT "Molecular cloning of chicken vasoactive intestinal polypeptide
RT receptor complementary DNA, tissue distribution and chromosomal

```

RT	localization."	Biol. Reprod.	64:1575-1581(2001).	EMBL	AB029895; BAA95164.1; "	GO	GO:0016020; F-G-protein coupled receptor activity; IEA.	GO	GO:0004930; F-g-protein coupled receptor activity; IEA.	GO	GO:0004872; F-receptor activity; IEA.	InterPro	IPR000832; GPCR_secretin.	PFam	PF00002; 7tm_2; 1.	PRINTS	PR00249; GPCRSECRETIN.	SMART	SM00008; Horms_1.	PROSITE	PS00649; G_PROTEIN_RECP_F2_1; 1.	PROSITE	PS00650; G_PROTEIN_RECP_F2_2; 1.	PROSITE	PS0227; G_PROTEIN_RECP_F2_3; 1.	PROSITE	PS0261; G_PROTEIN_RECP_F2_4; 1.	KW	Receptor.	FT	NON_TER	SEQUENCE	418 AA; 48191 MW; 7AE4796ADCB08FF3 CRC64;	Query Match	47.08; Score 1100; DB 13; Length 418;	Best Local Similarity	52.08; Pred. No. 6.5e-92;	Matches	220; Conservative	65; Mismatches	118; Indels	20; Gaps	97;																																																									
QY	29	LEIQRETKC-AELLRSOTEKHKACSGWNIITCWRPANVGETVTVPCKPVFSNFYSKAG	87	DB	3	LEIEERSQCLAL--TEDNQTSCRRQNDITCWPEAOVGAVVVKCPKFKRLTTLFLG	60	QY	88	NISKNCITSDGWSFTFP-DFVDAGY---SPDESKITFYILVKAIYTLGYSVSLMSLAT	143	DB	61	NVSRNCTSQGWTVDYPAPYAVACGYDSNSTPGE--QTAFYGTAKTGYTIGHTLSLIALLTA	119	QY	144	GSIIICLFRKLHCTRNVIHNLFLSFILRAISLVAKDDLVSSSGTLHCCPDQPSGWSVCK	203	DB	120	AMTIFCLFRKLHCTRNVIHMLFMSFIMRAVFIKQIVFESGEPEHC---FVSSVCK	176	QY	204	LSLVFQYCIYMANFFFWLLVGLYHLTLIV--AMLPFRRCFLAYLLIGWLGLPTVCIGAWTAA	262	DB	177	AMMVFFQYCVANFFFWLLVGLYHLTLIVSFSSERKVFWMYILIGWGPSVFITAWTV	236	QY	263	RLVLEDTGCDWTDNDHSYVPMWVIRPILISIVNVLFIISIRILLOKLTSPDVGNDQSO	322	DB	237	RIYFNVGVCWEETIETPFIIMIKPILVSLVNFILFICIIIRILVQKLHSDPDVGHNETSQ	296	QY	323	YKRLAKSTLLIPLFGVHYVMVAFVFPISISSKYQILFELCHGSGQLVAVLYCFINSEV	382	DB	297	YSRLAKSTLLIPLFGIHYIMFALFPDNFKAEVKLVELVVGSGQGVVAVLYCFINSEV	356	QY	383	QCELRKRWRCPTSPASRDYRVCGSFSRNGSEALQFH-----RGSRAQSFLQET	435	DB	357	QAELEKRWRRWHLEFRFGSDMKYHHPSSGSGNTNFSTQISMLTKCSPKTRRCSSP-QAEF	415	QY	436	SVI	438	DB	416	SLV	418	RESULT 8	Q802T7	PRELIMINARY;	PRT;	434 AA.	ID	Q802T7	Q802T7	AC	Q802T7	DT	01-JUN-2003	(TrEMBLrel. 24, Created)	DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)	DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	DE	Vasoactive intestinal peptide receptor.	GN	VIPR2A.	OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	OC	Tetraodontidae; Tetraodontidae; Takifugu.	OX	NCBI_TaxID=31033;	RN	[1]

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RP SEQUENCE FROM N.A.
RA Cardoso J.C.R.; Power D.M., Elgar G., Clark M.S.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cardoso J.C.R., Power D.M., Elgar G., Clark M.S.;
RT "Isolation and characterisation of the secretin receptor family
RL members in Fugu rubripes.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN EMBL; A4708877; CAC83860.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 434 AA; 49569 MW; A9D49C7A8E436CE2 CRC64;
Query Match 46.9%; Score 1099; DB 13; Length 434;
Best Local Similarity 52.5%; Pred. No. 8.4e-92;
Matches 212; Conservative 63; Mismatches 125; Indels 4; Gaps 3;
Qy 18 VNSIHPECRPHLEIQBEETKCAELLRSQTEKKKACSGWMDNITCWRPANVGETVIVCPK 77
Db 10 VHGKFPHCQFYWEMQARRDCQIQLORETSAHTGRCGEWMDVNSCWQSAAVGEVTTLP 69
Qy 78 VFNFYSKAGNISKNCTSDGSETFPDFVDACGVSDEDESKITFYILVKAITYLGYSVS 137
Db 70 PLJHLFGKGNLERTCTEAGWSEVVPATVACWSDNTDQPSSELLFYRVVKILSLGHSL 129
Qy 138 LMSIATGSIILCFRKLHCTRNVIHNLFLSFILRAISLVIKDVLVSSSGTLCPCDQPS 197
Db 130 LVTLITSTFMCFRRLHCTRNVIHNLVFSFMLRAVAVLAKDTLLFSDDETTDCSTQ 188
Qy 198 SWVGCKSLVFLQYCIANFVLLVEGLYHLTLIVAMLPFRCLAYLLIGWGLPTVCIG 257
Db 189 SLVGCKAILYFFNYFVNANFWLLVEGLYHLTLILLIRNASIRLUFVYMLIWGIPFF 248
Qy 258 AWTAAARLYEDTGCDWNDSVPWVIRIPILISIIIVNFVLFISIRILLQKLTSPDVGG 317
Db 249 AWICRVNLEDTRCWENNEPVNRLINWPIMASVINFFISIRILVQKLCQADVGG 308
Qy 318 NDGSQYKRLAKSTLLLLPLFGVHVMFAVF-PTGISKY-QILFELCLGSFQGLVAVL 374
Db 309 NEQSQFRLAKSTLLPLFGINVVVFVYMMPEPSDTNLYVKIIFELGLGSFQGLVAVL 368
Qy 375 YCFINSVQCELKWKESRCPTSPASRDYRVCGSSFSRNGSEGA 418
Db 369 YCFINSVQSELRRNGRSLSKRVGRDYKLUHAASAPNGGESS 412
RESULT 9
Q90Y07 PRELIMINARY; PRT; 480 AA.
AC Q90Y07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pituicary adenylyate cyclase-activating polypeptide receptor variant
DE PAC1-R25;
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8406;
RN [1]

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DE Pituitary adenylate cyclase-activating polypeptide receptor variant  
 DE PAC1-Rmc.  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Alexandre D., Vaudry H., Carpentier V., Fournier A., Jegou S.,  
 RA Anouar Y.;  
 RT "Novel Splice Variants of Pituitary Adenylate Cyclase-Activating  
 RT Polypeptide Type I Receptor in Frog Exhibit Altered G-Protein  
 RT Coupling";  
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF312683; AAL26838.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000832; GPCR secretin.  
 DR InterPro; IPR001879; hormu\_receptor.  
 DR Pfam; PF00002; 7tm\_2; 1.  
 DR PRINTS; PF02793; HRM; 1.  
 DR SMART; SM00008; Hormr; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS00227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS00261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 KW Receptor.  
 SQ SEQUENCE 465 AA; 53295 MW; E996B70A37DC23A9 CRC64;

Query Match 45.1%; Score 1056.5; DB 13; Length 465;  
 Best Local Similarity 50.8%; Pred. No. 6.8e-88;  
 Matches 203; Conservative 64; Mismatches 96; Indels 37; Gaps 9;  
 QY 9 LITCWLAPVNS-----IHPECRHLIEQBEETKCAEL-----LRSQTEKHKACSGWDN 58  
 DB 4 LLRLYLILLVASSILMAVMHPYC-----VIKBEETCLEKIQLELMWNDSMPGCGPMWDN 59  
 QY 59 ITCWRPANVGETVTPCKVPS-----NFYSK-----AGNISKNCTSDGWSSTEDFV 106  
 DB 60 ITCWPAVGVKAVIRCAWFSMDSDGMDPYDREHLEGVISGENTENGWSPPHYIS 119  
 QY 107 DACGY----SDPEDESKITFYLVKAIYTLGYSLMSLATGSIILCLFRKLHCTRYIH 162  
 DB 120 DACGFDVNETGDDQD---TYFLSVKALYTVGYSTSLVATTAMVILCKRKLHCTRNFIH 176  
 QY 163 LNLFLSFILRAISVLVDVLYSSSGTLHCDDQSSWGCKLSLVFLQYCTIMANFFLLV 222  
 DB 177 MNLFVSFILRAISVFIKDEVLYASQDSNHC---HVSTVEKAVMVFFHYCVMSNYFWLFI 233  
 QY 223 EGLYLHTLVV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCWDNDHSPVW 281  
 DB 234 EGLYLVLTVEFTFPERYFYWYIILGWGTPLICVTIWAVALRHFDGDCWEMNNVALW 293  
 QY 282 WVIPRLISIVNPLVFISIRILLQKLTSPDVGNDDQSQVKRIAKSTLLILPLFGVHY 341  
 DB 294 WVIKGPVLASIMINFLVFGIILVQKLQSPDIGNNESSYLRILARSTLLILPLFGHY 353  
 QY 342 MVFAVFPFISISSKYQILFELCLGSGFQGLVAVLYCFLNSE 381  
 DB 354 TVFAFSPENVSKRRLVFLGLGSGFQGLVAVLYCFLNGE 393

RESULT 14  
 Q8AXV4 PRELIMINARY; PRT; 419 AA.  
 ID Q8AXV4;  
 AC Q8AXV4;  
 DT 01-MAR-2003 (TremBLrel. 23, Created)  
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
 DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor  
 DE (Fragment).  
 OS Ovis aries (Sheep).  
 GN VIPR1B.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;  
 RA "Isolation and characterisation of the VIPR/PACAP receptor gene family  
 RT in Fugu rubripes";  
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296143; CAC82587.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000832; GPCR secretin.  
 DR InterPro; IPR001879; hormu\_receptor.  
 DR Pfam; PF00002; 7tm\_2; 1.  
 DR PRINTS; PF02793; HRM; 1.  
 DR SMART; SM00008; Hormr; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_1; 1.  
 DR PROSITE; PS00649; G\_PROTEIN\_RECEP\_F2\_2; 1.  
 DR PROSITE; PS00227; G\_PROTEIN\_RECEP\_F2\_3; 1.  
 DR PROSITE; PS00261; G\_PROTEIN\_RECEP\_F2\_4; 1.  
 KW Receptor.  
 SQ SEQUENCE 419 AA; 47662 MW; 0B7A764B53BA2A7E CRC64;

Query Match 44.4%; Score 1041; DB 13; Length 419;  
 Best Local Similarity 50.5%; Pred. No. 1.6e-86;  
 Matches 203; Conservative 60; Mismatches 125; Indels 14; Gaps 6;  
 QY 25 CRFHLIEQBEETKCAELLRSQTEKHKACSGWDNITCWRPANVGETVTPCKP--VFSNF 82  
 DB 2 CDMAELTEBEKDTCEAQIENKT---AGCTGMWDKITCWPSSADVGEVTVPCVLPFFSG 58  
 QY 83 YSKAGNISKNCTSDGWSSTEDFVDAGY---SDPEDESKITFYLVKAIYTLGYSLMS 139  
 DB 59 NTHLSNLKCTCTEDGWSPISDYTEDCGYDFNTVGDREAGFFSAIKVGYTVGHSVLI 118  
 QY 140 SLATGSIILCLFRKLHCTRYIHNLFLSILRAISVLVDVLYSSSGTLHCDDQSSW 199  
 DB 119 SLTIGIILCLFRKLHCTRYIHNLFLSILRAISVLVDVLYSSSGTLHCDDQSSW 174  
 QY 200 VGCKLSLVFLQYCTIMANFFLLVEGLYHLLV-AMLPFRRCFLAYLLIGWGLPTVCIGA 258  
 DB 175 VGCKAVMAPHYGIMASFFWLLVEGLYHLLVAVSFSEKRYFWGYTILGWGAPSVFISA 234  
 QY 259 WTAARLYLEDTCWDNDHSPVWVIRIPILISIVNPLVFISIRILLQKLTSPDVGN 318  
 DB 235 WVLTKAYLNDPGCWELIIDTL-NWIIKTPILGTLVNFILFIRILRQKNCPCDIGRR 293  
 QY 319 DQSOYKRLAKSTLLILPLFGVHVMVFAVFPFISISSKYQILFELCLGSGFQGLVAVLYCFL 378  
 DB 294 ESHQYSLAKSTLLILPLFGVHVMVFAVFPFISISSKYQILFELCLGSGFQGLVAVLYCFL 353  
 QY 379 NSVQCEKLRKWRSCRPTPSASRDYRVCGSFSFNSGEGALQ 420  
 DB 354 NGEVQAEIKRWRWRMLQRFGLGADTKYQPSIGSGNNGNFTQ 395

RESULT 15  
 Q8WMRO PRELIMINARY; PRT; 374 AA.  
 ID Q8WMRO;  
 AC Q8WMRO;  
 DT 01-MAR-2002 (TremBLrel. 20, Created)  
 DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)  
 DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor  
 DE (Fragment).  
 OS Ovis aries (Sheep).  
 GN VIPR1B.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:54:54 ; Search time 20 Seconds  
(without alignments)  
2106.594 Million cell updates/sec

Title: US-09-983-000A-20  
Perfect score: 2342  
Sequence: 1 MRTLPPALLTCWLLAPVNS.....LQFHGRSRAQSFQETQTSVI 438

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: piri:\*  
2: piri2:\*  
3: piri3:\*  
4: piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2342	100.0	438	2 G02822	vasoactive intesti
2	2032	86.8	437	2 S39069	vasoactive intesti
3	2030	86.7	437	2 J00185	PACAP/VIP receptor
4	1153.5	49.3	467	2 JN0616	pituitary adenylat
5	1150	49.1	525	2 JN0902	pituitary adenylat
6	1129.5	48.2	495	2 S36114	pituitary adenylat
7	1127.5	48.1	513	2 S47631	pituitary adenylat
8	1127.5	48.1	513	2 S47631	pituitary adenylat
9	1115.5	47.6	523	2 S39060	pituitary adenylat
10	1084.5	45.5	459	2 JH0594	vasoactive intesti
11	1024	43.7	460	2 J02194	vasoactive intesti
12	1018	43.5	449	2 J02195	vasoactive intesti
13	997.5	42.6	449	2 S16319	secretin receptor
14	992.5	42.4	440	2 J02532	secretin receptor
15	991	42.3	381	2 S33449	pituitary adenylat
16	879.5	37.6	423	2 A45363	somatoliberin rece
17	873.5	37.3	451	2 I46586	growth hormone-rel
18	846.5	36.1	423	2 S29753	growth hormone-rel
19	840.5	35.9	464	2 S29754	growth hormone-rel
20	760.5	32.5	585	2 A39286	parathyroid hormon
21	759	32.4	593	2 A49191	parathyroid hormon
22	754.5	32.2	591	2 S44203	parathyroid hormon
23	754.5	32.2	591	2 I54195	parathyroid hormon
24	738.5	31.5	589	2 I59297	parathyroid hormon
25	707	30.2	550	2 A57519	parathyroid hormon
26	701.5	30.0	462	2 J02462	gastric inhibitory
27	688.5	29.4	455	2 I53273	gastric inhibitory
28	674.5	28.8	463	2 A46172	glucagon-like pept
29	670	28.6	466	2 S66676	glucose-dependent

30	669	28.6	466	2 G02234	gastric inhibitory
31	666.5	28.5	477	2 JC2041	glucagon receptor
32	657.5	28.1	463	2 S71624	glucagon-like pept
33	650.5	27.8	485	2 J01957	glucagon receptor
34	646.5	27.6	463	2 I84494	glucagon-like pept
35	646.5	27.6	491	2 I37411	glucose-dependent
36	643	27.5	485	2 JC4363	glucagon receptor
37	489	20.9	415	2 S39535	corticotropin-rele
38	484	20.7	415	2 I58144	corticotropin-rele
39	483	20.6	431	2 I49279	sauvagine/corticot
40	482	20.6	411	2 A55610	corticotropin-rele
41	479	20.5	431	2 I49149	CRF receptor-mou
42	475.5	20.3	430	2 A56726	corticoliberin rec
43	459.5	19.6	444	2 A48260	corticoliberin rec
44	455.5	19.4	515	2 I49154	calcitonin recepto
45	447	19.1	482	2 A39285	calcitonin recepto

ALIGNMENTS

RESULT 1

G02822  
vasoactive intestinal peptide receptor 2 - human

C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 20-Jun-2000  
C;Accession: G02822; JC2463  
R;Lutz, E.M.  
submitted to the EMBL Data Library, January 1996

A;Reference number: H01736  
A;Accession: G02822  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-438 <LUT>

A;Cross-references: EMBL:X95097; NID:g1160469; PIDN:CAA64474.1; PID:g1160470

R;Svoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbroe

Biochem. Biophys. Res. Commun. 205, 1617-1624, 1994

A;Title: Molecular cloning and functional characterization of a human VIP receptor from

A;Reference number: JC2463; MUID:95110300; PMID:7811244

A;Accession: JC2463

A;Molecule type: mRNA

A;Residues: 1-38, 'T', 40-411, 'H', 413-423, 'A', 425-438 <SVO>

A;Cross-references: GB:I36566; NID:G550477; PIDN:AC37569.1; PID:G550478

A;Experimental source: SUP-T1 lymphoblast cell line

C;Genetics:

A;Gene: GDB:VIPR2

A;Cross-references: GDB:335025

A;Map position: 7q36.3-7q36.3

C;Superfamily: Glucagon receptor

C;Keywords: Glycoprotein; intestine; receptor; transmembrane protein

F;130-150/Domain: transmembrane #status predicted <TM1>

F;160-179/Domain: transmembrane #status predicted <TM2>

F;206-228/Domain: transmembrane #status predicted <TM3>

F;241-262/Domain: transmembrane #status predicted <TM4>

F;282-304/Domain: transmembrane #status predicted <TM5>

F;329-349/Domain: transmembrane #status predicted <TM6>

F;361-384/Domain: transmembrane #status predicted <TM7>

F;58,88,92/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 2342; DB 2; Length 438;

Best Local Similarity 100.0%; Pred. No. 1.7e-186;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWDNIT 60

Db 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWDNIT 60

Qy 61 CWRPNVGETVTPCPKVFNSFYSGKAGNISKNCTSDGSETFPDFVDACGSDPEDESKI 120

Db 61 CWRPNVGETVTPCPKVFNSFYSGKAGNISKNCTSDGSETFPDFVDACGSDPEDESKI 120

Qy 121 TFYLIVAKIYTLGVSVLSMSLATSIIICLPKRLCHTRNYIHLNLFSEILRAISVLVKD 180



Db 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVKD 180  
Qy 181 DVLVSSGTLHCPDPSSWGCKLSLFLVQYICIMANFWLLVEGLYHLLVAMLPERRC 240  
Db 181 DVLVSSGTLHCPDPSSWGCKLSLFLVQYICIMANFWLLVEGLYHLLVAMLPERRC 240  
Qy 241 FLAVLLIGWGLPTVCIGAWTAARLYLEDTGCDNDHSDVPMWVIRIPILISIVNFVLI 300  
Db 241 FLAVLLIGWGLPTVCIGAWTAARLYLEDTGCDNDHSDVPMWVIRIPILISIVNFVLI 300  
Qy 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFE 360  
Db 301 SIIRILLQKLTSPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFE 360  
Qy 361 LCLGSFQGLVAVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGLQ 420  
Db 361 LCLGSFQGLVAVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGLQ 420  
Qy 421 FHRGSRQSFLOTETSVI 438  
Db 421 FHRGSRQSFLOTETSVI 438

RESULT 2  
S39069  
Query Match 86.8%; Score 2032; DB 2; Length 437;  
Best Local Similarity 87.4%; Pred. No. 8.3e-161;  
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 08-Oct-1999  
C;Accession: J39069  
R;Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.  
FEBS Lett. 334, 3-8, 1993  
A;Title: The VIP(2) receptor: molecular characterization of a cDNA encoding a novel receptor  
A;Reference number: S39069; MUID:94039806; PMID:8224221  
A;Accession: J39069  
A;Molecule type: mRNA  
A;Residues: 1-437 <LUT>  
A;Cross-references: EMBL:Z25885; NID:G414188; PIDN:CAA81104.1; PID:G414189  
C;Superfamily: Glucagon receptor  
C;Keywords: G protein-coupled receptor; intestine; transmembrane protein

Qy 12 CWWLAPVNSIHPECRPHLEIQEBETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71  
Db 11 CWWLVRSIIHPECRPHLEIQEBETKCAELLSSQWENHRACSGVMDNITCWRPADIGTV 70  
Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETPPDFVDCGYSDPDESKITFYILVKAIYT 131  
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETPPDFIDACGYNDPDESKITFYILVKAIYT 130  
Qy 132 LGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVKDDVLYSSGTLH 191  
Db 131 LGYSVLSMLTGSIIILCLFRKLHCTRYIHNLFLSFMLRAISVLVKDVLVSSGSLR 190  
Qy 192 CPDOPSSWGCKLSLFLVQYICIMANFWLLVEGLYHLLVAMLPERRCFLAYLILGWGL 251  
Db 191 CHDOPSSWGCKLSLFLVQYICIMANFWLLVEGLYHLLVAILPPRCFLAYLILGWGI 250  
Qy 252 PTVCIGAWTAARLYLEDTGCDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 311  
Db 251 PSVCIGAWTAARLYLEDTGCDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 310  
Qy 312 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 371  
Db 311 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 370  
Qy 372 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGLQPHRGSRAQSFL 431  
Db 371 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGLQPHRGSRTQSFL 430  
Qy 432 QTETSVI 438  
Db 432 QTETSVI 438

Db 431 QSETSVI 437  
RESULT 3  
JU0185  
Query Match 86.7%; Score 2030; DB 2; Length 437;  
Best Local Similarity 87.4%; Pred. No. 1.2e-160;  
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 05-Nov-1999  
C;Accession: A53471; JU0185  
R;Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;  
Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994  
A;Title: Cloning and functional characterization of a third pituitary adenylylate cyclase  
A;Reference number: A53471; MUID:94195806; PMID:8146174  
A;Accession: A53471  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-437 <RES>  
A;Cross-references: GB:D28132; NID:G473721; PIDN:BAA05674.1; PID:G496376  
A;Experimental source: strain C57BL/6  
C;Superfamily: Glucagon receptor  
C;Keywords: receptor

Qy 12 CWWLAPVNSIHPECRPHLEIQEBETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71  
Db 11 CWWLVRSIIHPECRPHLEIQEBETKCAELLSSQWENHRACSGVMDNITCWRPADIGTV 70  
Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETPPDFVDCGYSDPDESKITFYILVKAIYT 131  
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETPPDFIDACGYNDPDESKITFYILVKAIYT 130  
Qy 132 LGYSVLSMLATGSIILCLFRKLHCTRYIHNLFLSFILRAISVLVKDDVLYSSGTLH 191  
Db 131 LGYSVLSMLTGSIIILCLFRKLHCTRYIHNLFLSFMLRAISVLVKDVLVSSGSLR 190  
Qy 192 CPDOPSSWGCKLSLFLVQYICIMANFWLLVEGLYHLLVAMLPERRCFLAYLILGWGL 251  
Db 191 CHDOPSSWGCKLSLFLVQYICIMANFWLLVEGLYHLLVAILPPRCFLAYLILGWGI 250  
Qy 252 PTVCIGAWTAARLYLEDTGCDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 311  
Db 251 PSVCIGAWTAARLYLEDTGCDNDHSDVPMWVIRIPILISIVNFVLI FISTIRILLOKLT 310  
Qy 312 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 371  
Db 311 SPDVGNDQSOYKRLAKSTLLLLPLFGVHYVMVFAVFPISISSKYQLIFECLGSFQGLV 370  
Qy 372 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGLQPHRGSRAQSFL 431  
Db 371 AVLYCFLNSVQCELRKWRRCPTPSASRDYRVCGSSFSRNGSEGLQPHRGSRTQSFL 430  
Qy 432 QTETSVI 438  
Db 431 QSETSVI 437

RESULT 4  
JU0616  
Query Match 86.8%; Score 2032; DB 2; Length 437;  
Best Local Similarity 87.4%; Pred. No. 8.3e-161;  
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
C;Accession: JN0616; S36768  
R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; Arin  
Biochem. Biophys. Res. Commun. 194, 133-143, 1993  
A;Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor  
A;Reference number: JN0616; MUID:93326107; PMID:7687425  
A;Accession: JN0616  
A;Molecule type: mRNA

A;Residues: 1-467 <HOS>  
 A;Experimental source: brain  
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; J.  
 Nature 365, 170-175, 1993  
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor.  
 A;Reference number: S36768; MUID:93382505; PMID:8396727  
 A;Accession: S36768  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-467 <SPE>  
 A;Cross-references: EMBL:Z23279; NID:g404252; PIDN:CAA80817.1; PID:g404253  
 C;Superfamily: glucagon receptor  
 C;Keywords: alternative splicing; glycoprotein; receptor  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-467/Product: pituitary adenylate cyclase-activating polypeptide receptor 46-5 #stat  
 F;47,59,116,299,342,374/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.3%; Score 1153.5; DB 2; Length 467;  
 Best Local Similarity 49.7%; Pred. No. 6.3e-88;  
 Matches 226; Conservative 63; Mismatches 127; Indels 39; Gaps 6;

QY 10 LTCMLAPVNSIHPECREHLEIOEETKCAEL-----LRSQTEKHKACGVDNDITCWR 63  
 Db 9 LTALLPVAIAHSDCIF-----KKEQAMCLERIQRANDLMGLNESSPGCPGMDNDITCWR 64  
 QY 64 PANVGETVTPCPKVFNSF-----YSKAGNISKNCTSDGWS 100  
 Db 65 PAQVGEMVLVSCPEVRIENPDQVMTETIGDSGFADNSLEITDMGVVGRNCTEDGWS 124  
 QY 101 TPDFVDACGYSD--PEDESKITFYILVKAITYLGVSLSLMSLATGSIILCLFRKHCHTR 158  
 Db 125 PPHFYDAGCFDYEPEGSDQDYVYLSVKALYTVGVYSTSLATTAMVILCRERKLHCTR 184  
 QY 159 NYLHNLFIILRAISLVKVDVLYSSSGTLCPCPOPSWCKLSLFLQYICIMANF 218  
 Db 185 NFTHMLVFSFMURASVFIKOWILYAEQDSHC---FVSTVECKAVMVFHYCVVSNYF 241  
 QY 219 WLIVEGLYLHTLLV-AMLPFRCLFAYLATIGWLGLPTVCIGAWTAARLYLEDTCGWDNDH 277  
 Db 242 WLFIEGLYLTLLVETFPFERRFYWYTIIGWGTPTVCVTWAVRLYFDDAGCWDND 301  
 QY 278 SVPMWIRPILLISIVNVLFTSIIRILLOKLTSPDVGGDOSQYKRLAKSLTLLIPLF 337  
 Db 302 TALMWIKGVGWSIMVNFVLTGIIILVQKLSQPDMDGNESSIYLRARSLLTLLIPLF 361  
 QY 338 GVHYMVFAVFPPISSKYQLFELCLGSGFGLVAVLYCFNLSEVOCELKRWKRSRCP 397  
 Db 362 GIHYTVAFSPENVSRRERLVFELGSGFGFVAVLYCFNLSEVOQAEIKRWKRSWKVR 421  
 QY 398 SASRDYRVCSSFRNGSEGALQFHRGSAQSLQ 432  
 Db 422 YFTMDFKRHPSLASSGVNGGTQLSILSKSSQLR 456

RESULT 5  
 pituitary adenylate cyclase activating peptide receptor type I precursor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Jun-2000  
 C;Accession: JN0902  
 R;Ogi, K.; Miyamoto, Y.; Masuda, Y.; Habata, Y.; Hosoya, M.; Ohtaki, T.; Masuo, Y.; Onda  
 Biochem. Biophys. Res. Commun. 196, 1511-1521, 1993  
 A;Title: Molecular cloning and functional expression of a cDNA encoding a human pituita  
 A;Reference number: JN0902; MUID:94071918; PMID:7902709  
 A;Accession: JN0902  
 A;Molecule type: mRNA  
 A;Residues: 1-525 <OGI>  
 A;Cross-references: DDBJ:DJ7516; NID:g457562; PIDN:BA044466.1; PID:g540518  
 A;Experimental source: pituitary  
 C;Comment: This protein plays pivotal roles as a neurotransmitter and a neuromodulator.  
 C;Superfamily: glucagon receptor  
 C;Keywords: glycoprotein; neurotransmitter; receptor  
 F;1-77/Domain: signal sequence #status predicted <SIG>

F;78-525/Product: pituitary adenylate cyclase activating peptide receptor type I #statu  
 F;105,117,174,357,400,432/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.1%; Score 1150; DB 2; Length 525;  
 Best Local Similarity 48.2%; Pred. No. 1.4e-87;  
 Matches 225; Conservative 68; Mismatches 118; Indels 56; Gaps 7;

QY 12 CW-----LLAPVNSIHPECREHLEIOEETKCAELLSQTE-----K 48  
 Db 52 CUPRSVMAGVHVSLAALLLPAPAMHSDCIF-----KKEQAMCLERIANELMCFNDS 107  
 QY 49 HKACGVDNDITCWRPANVGETVTPCPKVFNSF-----YSK 85  
 Db 108 SPGCPGMDNDITCWRPAHVGEMVLVSCPELFRIFNPDQVMTETIGESDFGDSNSLDLSD 167  
 QY 86 AGNISKNCTSDGWSSTETPDFVDACGYSDPEDES--KITFYILVKAITYLGVSLSLMSLAT 143  
 Db 168 MGVSGRNCTEDGWSBEPFFHYDACGFDEYESTGDDYIYLSVKALYTVGVYSTSLVTLTT 227  
 QY 144 GSIIILCLFRKLHCTRNYIHLNLFILRAISLVKVDVLYSSSGTLCPCPOPSWVGCK 203  
 Db 228 AMVILCRERKLHCTRNFHMLNLFVSPMLRAISVFIKOWILYAEQDSNHC---FISTVECK 284  
 QY 204 LSLVFLQYICIMANFVLLVEGLYLHTLLV-AMLPFRCLFAYLATIGWLGLPTVCIGAWTA 262  
 Db 285 AVMVFFHYCVVSNYFVLFIEGLYLTLLVETFPFERRFYWYTIIGWGTPTVCVTWATL 344  
 QY 263 RLYLEDTCGWDNDHSPMWIRPILLISIVNVLFTSIIRILLOKLTSPDVGGDOSQ 322  
 Db 345 RUYFDTCGWDNDSTALMWIKGVGWSIMVNFVLTGIIILVQKLSQPDMDGNESSI 404  
 QY 323 YKRLAKSLTLLIPLFGVHYMVFAVFPPISSKYQLFELCLGSGFGLVAVLYCFNLSEV 382  
 Db 405 YLRARSLLTLLIPLFGIHYTVAFSPENVSRRERLVFELGSGFGFVAVLYCFNLSEV 464  
 QY 383 QCELKRWKRSRCPETPSASRDYRVCSSFRNGSEGALQFHRGSAOS 429  
 Db 465 QAEIKRWKRSWKVRNYFAVDKFRHPSLASSGVNGGTQLSILSKSS 511

RESULT 6  
 pituitary adenylate cyclase-activating polypeptide type I receptor precursor - rat  
 N;Alternate names: PACAP receptor  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-2000  
 C;Accession: S36114; JN0617; S39062; S39063; PNO608; PNO609; I58147; A48204  
 R;Morrow, J.A.; Lutz, E.M.; West, K.M.; Fink, G.; Harmar, A.J.  
 FEBS Lett. 329, 99-105, 1993  
 A;Title: Molecular cloning and expression of a cDNA encoding a receptor for pituitary  
 A;Reference number: S36114; MUID:93359075; PMID:8394834  
 A;Accession: S36114  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-495 <MOR>  
 A;Cross-references: EMBL:Z23282; NID:g397520; PIDN:CAA80820.1; PID:g397521  
 R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; Ari  
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993  
 A;Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor  
 A;Reference number: JN0616; MUID:93326107; PMID:7687425  
 A;Accession: JN0617  
 A;Molecule type: mRNA  
 A;Residues: 1-495 <HOS>  
 A;Experimental source: brain  
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; S  
 Nature 365, 170-175, 1993  
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor:  
 A;Reference number: S36768; MUID:93382505; PMID:8396727  
 A;Accession: S39062  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-495 <SPE>  
 A;Cross-references: EMBL:Z23274; NID:g404220; PIDN:CAA80812.1; PID:g404221



Db 482 QLR 484

RESULT 8  
S47631  
pituitary adenylate cyclase-activating polypeptide type I receptor precursor - bovine  
N;Alternate names: PACAP receptor  
N;Contains: pituitary adenylate cyclase-activating polypeptide type I receptor long form  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Jun-2000  
C;Accession: S47631; MUID:94325336; PMID:8049255  
R;Miyamoto, Y.; Habata, Y.; Ohtaki, T.; Masuda, Y.; Ogi, K.; Onda, H.; Fujino, M.  
Biochim. Biophys. Acta 1218, 297-307, 1994  
A;Title: Cloning and expression of a complementary DNA encoding the bovine receptor for  
A;Reference number: S47631; MUID:94325336; PMID:8049255  
A;Accession: S47631  
A;Molecule type: mRNA  
A;Residues: 1-513 <MTY>  
A;Cross-references: EMBL:DL17290; NID:9602765; PIDN:BAA04122.1; PID:g1374682  
A;Experimental source: brain  
A;Accession: S47632  
A;Molecule type: protein  
A;Residues: 38-41, 'X', 43-50, 'X', 52-66 <MT2>  
A;Experimental source: brain  
C;Genetics:  
C;Introns: 366/2  
C;Function:  
A;Description: stimulates both adenylate cyclase and phospholipase C  
C;Superfamily: Glucagon receptor  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; phosphoprote  
F;1-37/Domain: signal sequence #status predicted <SIG>  
F;38-513/Product: pituitary adenylate cyclase-activating polypeptide type I receptor lon  
F;38-365,394-513/Product: pituitary adenylate cyclase-activating polypeptide type I rece  
F;173-195/Domain: transmembrane #status predicted <TM1>  
F;204-222/Domain: transmembrane #status predicted <TM2>  
F;245-270/Domain: transmembrane #status predicted <TM3>  
F;286-308/Domain: transmembrane #status predicted <TM4>  
F;326-349/Domain: transmembrane #status predicted <TM5>  
F;396-416/Domain: transmembrane #status predicted <TM6>  
F;431-451/Domain: transmembrane #status predicted <TM7>  
F;65,77,134,360,420/Binding site: carbonylate (Asn) (covalent) #status predicted  
F;383,462/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 48.1%; Score 1127.5; DB 2; Length 513;  
Best Local Similarity 45.8%; Pred. No. 9.9e-86;  
Matches 224; Conservative 72; Mismatches 126; Indels 67; Gaps 7;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIOBEETKCAEL-----LRQTEKHKACSG 54  
Db 18 MASIAQVSLAALLLPATAMHSDCIF---KKEQAMCLEIORVNDLMGINDSSPGCPG 73  
QY 55 VQDNITCWRPNYGETVTPCPKVSFNF-----YSKAGNISK 91  
Db 74 MWDNITCWKFAHGVMLVSCPELFRPNPDQWETETIGFPGADSKSLDLSMRVVS 133  
QY 92 NCTSDGSETFPDFVDACGSDPEDES--KITFYILVKAIYTLGYSVLSMLATGSIILC 149  
Db 134 NCTEDGWSEPPHYFDACGFEYESRGDQDYVYLSVKALYTVGYSTSLVTLITAMVILC 193  
QY 150 LFRKLHCTRYIHLNLFILRAISVLVVDVLYSSGTLHCPDQSPSSWGCKLSLVFL 209  
Db 194 RFRKLHCTRYIHLNLFVSMFLRAISVFIKDWILYAEQDSNHC---FVSTVECKAVMVFF 250  
QY 210 QYCIAMFFVLLVGLVHLTLV-AMLPPRCFLAYLLIGWGLPTVCIGAWTAARLYLED 268  
Db 251 HYCVSNYFVFLFGLVYLLVETFPFERRYFWYTIIGWGTPTVCVSVWMLRLYFDD 310  
QY 269 TGCWDTNDHSPVWVIRIPILISIVNVLFIISIRILLQKLTSPDVGNDQSQY----- 323  
Db 311 TGCWDMNDTALWVWIKGVPVGSIMVNVFLFIGIILVQKLSQSPDMGNESSIYFSCVQ 370  
QY 324 -----XRLAKSTLLILPLFGVHMVMPFAVFPFISISKYQILFE 360

Db 371 KCYCKPQRAQOQSKMSLSITILRLARSTLLILPLFGIHYTVFAFSPENVKRERIVFE 430  
QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRSCPTPSASRDYRVKVCSSFSRNGSEALQ 420  
Db 431 LGLGSFQGFVAVLYCFNLGEVQAEIKRWKRWKVNRYFTWDFKRRHPSLASSVNGGTQ 490  
QY 421 FHRGSRAQS 429  
Db 491 LSILSKSSS 499

RESULT 9  
S39060  
pituitary adenylate cyclase activating-peptide receptor form 2 - rat  
N;Alternate names: PACAP receptor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Nov-1999  
C;Accession: S39060  
R;Spengler, D.; Waeber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.;  
Nature 365, 170-175, 1993  
A;Title: Differential signal transduction by five splice variants of the PACAP receptor  
A;Reference number: S36768; MUID:93382505; PMID:8396727  
A;Accession: S39060  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-523 <SPE>  
A;Cross-references: EMBL:Z23272; NID:9404195; PIDN:CAA80810.1; PID:g404196  
C;Superfamily: Glucagon receptor

Query Match 47.6%; Score 1115.5; DB 2; Length 523;  
Best Local Similarity 44.3%; Pred. No. 1e-84;  
Matches 226; Conservative 63; Mismatches 127; Indels 95; Gaps 7;

QY 10 LTCWLLAPVNSIHPECRFHLEIOBEETKCAEL-----LRQTEKHKACSGWMDNITCWR 63  
Db 9 LTALLLPVALIAMEHSDCIF---KKEQAMCLEIORANDLMGLNESSPGCPGMDNITCWK 64  
QY 64 PANVGETVTPCPKVSFNF-----YSKAGNISKNCTSDQSE 100  
Db 65 PAQGVMLVSCPEVFRIFNPDPQWMTETIGDSGFADSNLEITDMGVVGRNCTEDGWE 124  
QY 101 TFPDFVDACGSD--PEDESKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTR 158  
Db 125 PPHYFDACGDDYEPESGDDYVYLSVKALYTVGYSTSLATLTAMVILCRFRKLHCTR 184  
QY 159 NYHLNLFILRAISVLVVDVLYSSGTLHCPDQSPSSWGCKLSLVFLQYCIAMNFF 218  
Db 185 NFTHMNLVSMFLRAISVFIKDWILYAEQDSNHC---FVSTVECKAVMVFFHYCVVSNYF 241  
QY 219 WLLVGLVYHLTLV-AMLPPRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDH 277  
Db 242 WLFEGLYLFTLLVETFPFERRYFWYTIIGWGTPTVCVTVAVLRLYFDAGCWMNDS 301  
QY 278 SVPWVIRIPILISIVNVLFIISIRILLQKLTSPDVGNDQSQY----- 323  
Db 302 TALWVWIKGVPVGSIMVNVFLFIGIILVQKLSQSPDMGNESSIYLTNLRVLPVKKTR 361  
QY 324 -----XRLAKSTLLILPLFGVHY 341  
Db 362 DPLVPFSDQHSPPFLSCVQKCYCKPQRAQOQSKMSLSITILRLARSTLLILPLFGIHY 421  
QY 342 MVFAVFPISISKYQILFELCLGSGFGLVAVLYCFNLSEVQCELRKWRSCPTPSASR 401  
Db 422 TVFAFSPENVKERLVLVFLGLGSGFGVAVLYCFNLGEVQAEIKRWKRWKVNRYFTM 481  
QY 402 DYKVCSSFSRNGSEALQFHRGSRAQSFLQ 432  
Db 482 DFKRRHPSLASSVNGGTQLSILSKSSS 512

RESULT 10  
JH0594

vasoactive intestinal peptide receptor precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C:Accession: JH0594; S56014  
 R: Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.  
 Neuron 8, 811-819, 1992  
 A:Title: Functional expression and tissue distribution of a novel receptor for vasoactive intestinal peptide  
 A:Reference number: JH0594; MUID:92232309; PMID:1314625  
 A:Accession: JH0594  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <ISH>  
 A:Cross-references: GB:M86835; NID:G207640; PIDN:AAA42331.1; PID:G207641  
 A:Experimental source: lung  
 R:Pei, L.; Melmed, S.  
 Biochem. J. 308, 719-723, 1995  
 A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'  
 A:Reference number: S56014; MUID:97104266; PMID:8948424  
 A:Accession: S56014  
 A>Status: preliminary; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-26 <PEI>  
 A:Cross-references: EMBL:U10635; NID:G505752; PIDN:AA848185.1; PID:G514311  
 C:Superfamily: Glucagon receptor  
 C:Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>  
 F:146-168/Domain: transmembrane #status predicted <TM1>  
 F:176-195/Domain: transmembrane #status predicted <TM2>  
 F:218-241/Domain: transmembrane #status predicted <TM3>  
 F:256-277/Domain: transmembrane #status predicted <TM4>  
 F:295-318/Domain: transmembrane #status predicted <TM5>  
 F:344-363/Domain: transmembrane #status predicted <TM6>  
 F:376-395/Domain: transmembrane #status predicted <TM7>  
 F:58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 45.5%; Score 1064.5; DB 2; Length 459;  
 Best Local Similarity 47.1%; Pred. No. 1.5e-80;  
 Matches 221; Conservative 68; Mismatches 139; Indels 41; Gaps 11;  
 QY 1 MRTLPP-----ALLTCWLLAPVN-----SIHPECFPHLEIQEEFKCABELLSQTE 47  
 Db 1 MRPPSPHVRWLCVLGALAC-ALRPAGSOASPOHECYLOLIEFQRCQCLEBAQLENE 59  
 QY 48 HKACSGVDNITCWRPANVGETVTVPCKVFSNFYSKAG-NISKNCTSDGMSFPP-DF 105  
 Db 60 T-TGCSKMDNLTCTWPTTPRGQAVLDCPLIFQLFAPIHGYNLSRSTEGNSQLEPGPY 118  
 QY 106 VDAGYSDP-----EDESKITFYLKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVI 161  
 Db 119 HTACGLNDRASLDEQQQTKFYNTVTKTYTIGYSLASLLVAMAILSLFRKLHCTRNVI 178  
 QY 162 HNLFLSFLIRALSVLKDDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCIWANFWLL 221  
 Db 179 HMLFMSFILRATAVFIKDMALFNSGEIDHCSB---ASVGCKAAVVFQYCVWANFWLL 235  
 QY 222 VEGLYLHTLL-VAMLPRRRCFLAYLLIGWGLPTVCIGAWTAARLXLEDTCGWDTHSV 280  
 Db 236 VEGLYLTLAVSFYSERKVFYNGYLLIGWVSVFTITVTVRIYFEDFGWDTHSV 295  
 QY 281 WVIIRIPILISIVNVLFIISIRILLQKLTSPDVGNDQSQYKRLAKSTLLILPLFGVH 340  
 Db 296 WIIKAPILLISLVNVLFIICIRILVQKLRPPDIGNDSFYSRLAKSTLLILPLFGIH 355  
 QY 341 YMVFAVFPISISKYQILFELCLGSGFQGLVAVLYCFLNSVQCELRKWR----- 391  
 Db 356 YVMAFFPDPNFAQVKNVVELVGSFGGFVAILYCFLNGEVOAELRRKWRHLLQGVIG 415  
 QY 392 --SRCTPTASRDYRVCGSFRNGSEGALQPHRGSAQSFLOQTETSVI 438  
 Db 416 WSSKSHPPWGGSGNGATCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 459

RESULT 11

JC2194  
 vasoactive intestinal peptide receptor precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 05-Nov-1999  
 C:Accession: JC2194; JN0604; PC2289; S38397  
 R: Couvineau, A.; Ruyter-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis, B.  
 Biochem. Biophys. Res. Commun. 200, 769-776, 1994  
 A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA  
 A:Reference number: JC2194; MUID:94235025; PMID:8179610  
 A:Accession: JC2194  
 A:Molecule type: mRNA  
 A:Residues: 1-460 <COU>  
 A:Cross-references: EMBL:X75299; NID:G407461; PIDN:CAA53046.1; PID:G407462  
 R:Experimental source: jejunal epithelial cell; clone HIVR8  
 R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.  
 Biochem. Biophys. Res. Commun. 193, 546-553, 1993  
 A:Title: Cloning and functional expression of a human neuroendocrine vasoactive intestinal peptide receptor  
 A:Reference number: JN0604; MUID:93290641; PMID:8390245  
 A:Accession: JN0604  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-284,288-460 <SRE>  
 A:Cross-references: GB:L13286; NID:G292903; PIDN:AAA36805.1; PID:G292904  
 R: Couvineau, A.; Gaudin, P.; Maoret, J.J.; Ruyter-Fessard, C.; Nicole, P.; Laburthe, M.  
 Biochem. Biophys. Res. Commun. 206, 246-252, 1995  
 A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-termina  
 A:Reference number: PC2289; MUID:95118345; PMID:7818527  
 A:Accession: PC2289  
 A:Molecule type: mRNA  
 A:Residues: 63-129 <CO2>  
 C:Genetics:  
 A:Gene: GDB:VIPR1; RCD1; HVR1  
 A:Cross-references: GDB:128589; OMIM:192321  
 A:Map position: 3p22-3p22  
 C:Superfamily: glucagon receptor  
 C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pr  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>  
 F:145-168/Domain: transmembrane #status predicted <TM1>  
 F:176-194/Domain: transmembrane #status predicted <TM2>  
 F:216-234/Domain: transmembrane #status predicted <TM3>  
 F:255-277/Domain: transmembrane #status predicted <TM4>  
 F:299-319/Domain: transmembrane #status predicted <TM5>  
 F:346-363/Domain: transmembrane #status predicted <TM6>  
 F:377-396/Domain: transmembrane #status predicted <TM7>  
 F:58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
 F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
 F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 Query Match 43.7%; Score 1024; DB 2; Length 460;  
 Best Local Similarity 46.0%; Pred. No. 3.4e-77;  
 Matches 216; Conservative 68; Mismatches 144; Indels 42; Gaps 13;  
 QY 1 MRTLPP-PALLATC-----WLLAPVNS-----IHPCECFHLEIQEEFKCABELLSQTEK 48  
 Db 1 MRPPSPHVRWLCVLGALAC-ALRPAGSOASPOHECYLOLIEFQRCQCLEBAQLENET 60  
 QY 49 HKACSGVDNITCWRPANVGETVTVPCKVFSNFYSKAG-NISKNCTSDGMSFPP-DFV 106  
 Db 61 -IGCSKMDNLTCTWPTTPRGQAVLDCPLIFQLFAPIHGYNLSRSTEGNSQLEPGPY 119  
 QY 107 DACGYSDP-----EDESKITFYLKAIYTLGYSVLSMLATGSIILCLFRKLHCTRNVI 163  
 Db 120 IACGLDDKAASLDEQQQTFYNGYLLIGWGLPTVCIGAWTAARLXLEDTCGWDTHSV 179  
 QY 164 HNLFLSFLIRALSVLKDDVLYSSSGTLHCPDQPSWVGCKLSLVFLQYCIWANFWLL 223  
 Db 180 HLFISFILRAAAVFIKDMALFNSGESDQCSB---GSVCKAAVVFQYCVWANFWLL 236  
 QY 224 GYLHLTL-VAMLPRRRCFLAYLLIGWGLPTVCIGAWTAARLXLEDTCGWDTHSV 279  
 Db 237 GLYLYTLAVSFYSERKVFYNGYLLIGWVSVFTITVTVRIYFEDFGWDTHSV 296



C;Accession: JC2532  
R;Jiang, S.; Ulrich, C.  
Biochem. Biophys. Res. Commun. 207, 893-890, 1995  
A;Title: Molecular cloning and functional expression of a human pancreatic secretin receptor  
A;Reference number: JC2532; MUID:95169147; PMID:7864894  
A;Accession: JC2532  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-440 <JIA>  
A;Cross-references: EMBL:U20178; NID:9662795; PIDN:AAC50106.1; PID:9662796  
A;Experimental source: pancreas  
C;Genetics  
A;Gene: SCTR  
A;Cross-references: GDB:270546; OMIM:182098  
A;Map position: 2q14.1-2q14.1  
C;Superfamily: glucagon receptor

Query Match 42.4%; Score 992.5; DB 2; Length 440;  
Best Local Similarity 47.9%; Pred. No. 1.3e-74;  
Matches 192; Conservative 72; Mismatches 122; Indels 15; Gaps 7;

Qy 1 MRTLPPALLICWLLAPVNSIHPCRFHELETOBETKC-ABELRSOT-----EKHKACS 53  
Db 9 LQQLLPVLLAC-AAHSTGALPRLCDVLQVLWESQDQCLQELSREQTGDLTGTEQVPVGC 67

Qy 54 GVNDNITCWRPANVGETVTPCKVFSNFYKAGNISKNTSDGWSETF--PDFVDACGY 111  
Db 68 GWNDNISCPSSVPGRMVECEPRFLMLTBRNGSLFRNCTQDQWSETFPRPNLACAVN 127

Qy 112 SDPEDESKITFYILKALTYGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLFSFIL 171  
Db 128 NDSSNEKRHSYLLKVMYTVGYSSSLVALLVALGILCAFRRLHCTRYNIHMLFVSPIL 187

Qy 172 RAISVLVQDDVLYSSSTGLHCPDQSPSSWGCKLSLVFYCYCIMANFFWLVLEGLYHLL 231  
Db 188 RALSNFIDAVLFSDDDVTYC---DAHRAGCKLVMLVFQCYCIMANYSWLVLEGLYHLL 244

Qy 232 -VAMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTGWDNDHSVPWWVIRIPILI 290  
Db 245 AIFSFSERKYLQGFVAFGWSGPAIFVALWATARHLEDVGCWDINANASIWWIRGPFIL 304

Qy 291 SIIVNVLFIPIIRILLQKLSPDVGGNDQSQYKRLAKSTLLPLFGVHYVMVFAVFPIS 350  
Db 305 SILINFILFINILIRILMKRLTQETRGNEVSHYKELARSTLLPLFGIHYIVFAFSP-E 363

Qy 351 ISSKYQILFELCLGSGFQGLVAVLYCFLNSENVCQELKRW 391  
Db 364 DAMEIQLFELALASFGLVAVLYCFLNGEVQLEVQKRW 404

RESULT 15  
S33449  
Pituitary adenylate cyclase-activating polypeptide receptor homolog - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000  
C;Accession: S33449  
R;Svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Christophe, J.  
submitted to the EMBL Data Library, May 1993  
A;Description: Molecular cloning of a PACAP-type receptor.  
A;Reference number: S33449  
A;Accession: S33449  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-381 <SVO>  
A;Cross-references: EMBL:Z22735; NID:9311228; PIDN:CAA80429.1; PID:9311229  
C;Superfamily: glucagon receptor

Query Match 42.3%; Score 991; DB 2; Length 381;  
Best Local Similarity 51.1%; Pred. No. 1.5e-74;  
Matches 192; Conservative 53; Mismatches 97; Indels 34; Gaps 4;

Qy 91 KNCTSDGWSSETPDFDAGCYSD--PEDESKITFYILKALTYGYSVLSMLATGSIIL 148

Db 1 RNCETDGSSEFFPHYFDACGDDYEPESGDQDYLLSWKALYTVGYSTSLATLTAMVIL 60  
Qy 149 CLFRKLHCTRYNIHLNPLFSILRAISVLVQDDVLYSSSTGLHCPDQSPSSWGCKLSLVF 208  
Db 61 CRFRKLHCTRYNIHLNPLFSILRAISVLVQDDVLYSSSTGLHCPDQSPSSWGCKLSLVF 117  
Qy 209 LQYCI MANFFWLVLEGLYHLLV-AMLPFRRCFLAYLLIGWGLPTVCIGAWTAARLYLE 267  
Db 118 FHYCVSNYFWLFEGLYHLLVETFFPERRYFYWTIIIGWGTPTVCVTWAVRLYFD 177  
Qy 268 DTGWDNDHSVPWWVIRIPILISIIIVNVLFIIRILLQKLSPTDVGGNDQSQY--- 323  
Db 178 DAGCWDNDSTALWVWIKGPVWGSIMVNFVFIGIILVQKLSQSPDMGNGESSIYFSCV 237  
Qy 324 -----KRLAKSTLLPLFGVHYVMVFAVFPISISSKYQILF 359  
Db 238 QKCYCKPQRAQHSCKMSLSLTITRLARSTLLPLFGIHYTVFAFSPENVSKRELIVF 297  
Qy 360 ELCLGSGFQGLVAVLYCFLNSENVCQELKRWSRCTPSPASRDYRVCGSGSFRNGSEGL 419  
Db 298 ELGLGSGFQGLVAVLYCFLNSENVCQELKRWSRKWRNRYFTMDFKRHPSPSLASSGVNGT 357  
Qy 420 QFHRGSRAGSFLQET 435  
Db 358 QLSILSKSSSHVRMST 373

Search completed: June 22, 2004, 08:59:33  
Job time : 21 secs

[illegible]

## ALIGNMENTS



Query Match 100.0%; Score 2342; DB 1; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1e-212;  
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQBEETKCAELLRSQTEKHKACSGVWDNIT 60  
DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQBEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPEDESKI 120  
DB 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPEDESKI 120

QY 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
DB 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180

QY 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLPERRC 240  
DB 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVFI 300  
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVFI 300

QY 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYVMFAVFPISISKYQILFE 360  
DB 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYVMFAVFPISISKYQILFE 360

QY 361 LCLGSFQGLVVAVLYCFINSEVOCELKRWRSRCPPTPSASRDYRVCGSSFSRNGSEGAQ 420  
DB 361 LCLGSFQGLVVAVLYCFINSEVOCELKRWRSRCPPTPSASRDYRVCGSSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438  
DB 421 FHRGSAQSFLQTETSVI 438

RESULT 2  
PCT-US01-08656-8498  
; Sequence 8498, Application PC/TUS0108656  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-066  
; CURRENT APPLICATION NUMBER: PCT/US01/08656  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-16  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 10994  
; SOFTWARE: Custom  
; SEQ ID NO 8498  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (133)..(179)  
; OTHER INFORMATION: G-protein coupled receptors family 2 proteins domain  
; OTHER INFORMATION: identified by eMATRIX, accession number BL00649B, p-value=9.625e-  
; OTHER INFORMATION: 38, raw score of 20.68  
; NAME/KEY: DOMAIN  
; LOCATION: (123)..(382)  
; OTHER INFORMATION: 7 transmembrane receptor (Secretin family) domain identified  
; OTHER INFORMATION: by Pfam, accession name 7tm\_2, E-value=8.8e-131, Pfam score of  
; OTHER INFORMATION: 447.9  
PCT-US01-08656-8498

Query Match 100.0%; Score 2342; DB 1; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1e-212;  
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQBEETKCAELLRSQTEKHKACSGVWDNIT 60  
DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQBEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPEDESKI 120  
DB 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPEDESKI 120

QY 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
DB 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180

QY 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLPERRC 240  
DB 181 DVLYSSGTLHCPDPQSSWGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVFI 300  
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIVNFVFI 300

QY 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYVMFAVFPISISKYQILFE 360  
DB 301 SIIRILLOKLTSPDVGGNDQSYKRLAKSTLLIPLFGVHYVMFAVFPISISKYQILFE 360

QY 361 LCLGSFQGLVVAVLYCFINSEVOCELKRWRSRCPPTPSASRDYRVCGSSFSRNGSEGAQ 420  
DB 361 LCLGSFQGLVVAVLYCFINSEVOCELKRWRSRCPPTPSASRDYRVCGSSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438  
DB 421 FHRGSAQSFLQTETSVI 438

RESULT 3  
US-09-631-603-24  
; Sequence 24, Application US/09631603  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; APPLICANT: Lloyd, Clare  
; APPLICANT: Weich, Nadine  
; TITLE OF INVENTION: 15571, A Novel GPCR-like Molecule of the  
; FILE REFERENCE: Secretin-Like Family and Uses Thereof  
; CURRENT APPLICATION NUMBER: US/09/631,603  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/515,781  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: 60/146,916  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-631-603-24

Query Match 100.0%; Score 2342; DB 20; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1e-212;  
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQBEETKCAELLRSQTEKHKACSGVWDNIT 60  
DB 1 MRTLPPALLTCWLLAPVNSIHPCRFHLEIQBEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPEDESKI 120  
DB 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVACGYSDPEDESKI 120

QY 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
DB 121 TFYILVKAIVTLGYSVSLMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180

QY 181 DVLSSSGTLHCPDOPSSWVGKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPBRC 240  
DB 181 DVLSSSGTLHCPDOPSSWVGKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPBRC 240  
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLI 300  
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLI 300  
QY 301 SIIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360  
DB 301 SIIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360  
QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420  
DB 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420  
QY 421 FHRGSAQSFLOTETSVI 438  
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 4  
US-09-694-519-10  
; Sequence 10, Application US/09694519  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/09/694,519  
; CURRENT FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: homo sapiens;  
US-09-694-519-10

Query Match 100.0%; Score 2342; DB 20; Length 438;  
Best Local Similarity 100.0%; Pred. No. 1e-212;  
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFLHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
DB 1 MRTLPPALLTCWLLAPVNSIHPECRFLHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
DB 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
QY 121 TFYIIVKAIYTLGYSVLSLMTAGSIILCLPKLHCTRYIHNLFLSFILRAISVLVKD 180  
DB 121 TFYIIVKAIYTLGYSVLSLMTAGSIILCLPKLHCTRYIHNLFLSFILRAISVLVKD 180  
QY 181 DVLSSSGTLHCPDOPSSWVGKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPBRC 240  
DB 181 DVLSSSGTLHCPDOPSSWVGKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPBRC 240  
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLI 300  
DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSPVWVIRIPILISIVNFVLI 300  
QY 301 SIIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360  
DB 301 SIIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360  
QY 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420  
DB 361 LCLGSFQGLVAVLYCFNLSEVQCELRKWRRCPTPSASRDYRVCGSFSRNGSEGALQ 420

QY 421 FHRGSAQSFLOTETSVI 438  
DB 421 FHRGSAQSFLOTETSVI 438

RESULT 5  
US-09-983-000a-20  
; Sequence 20, Application US/09983000A  
; GENERAL INFORMATION:  
; APPLICANT: AGY Therapeutics  
; APPLICANT: Melcher, Thorsten  
; APPLICANT: Mueller, Sabine  
; APPLICANT: Chin, Daniel  
; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUAL  
; FILE REFERENCE: 263/180 -- Peagleman -- AGY  
; CURRENT APPLICATION NUMBER: US/09/983,000A  
; CURRENT FILING DATE: 2001-10-17  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(23)  
; OTHER INFORMATION: Potential  
; NAME/KEY: GENE  
; LOCATION: (1)..(438)  
; OTHER INFORMATION: Vasoactive Intestinal Peptide Receptor 2  
; NAME/KEY: CHAIN  
; LOCATION: (24)..(438)  
; OTHER INFORMATION: Vasoactive Intestinal Polypeptide Receptor 2  
; NAME/KEY: DOMAIN  
; LOCATION: (24)..(126)  
; OTHER INFORMATION: 1 (Potential)  
; NAME/KEY: TRANSMEM  
; LOCATION: (127)..(151)  
; OTHER INFORMATION: 1 (Potential)  
; NAME/KEY: DOMAIN  
; LOCATION: (152)..(158)  
; OTHER INFORMATION: Cytoplasmic (potential)  
; NAME/KEY: TRANSMEM  
; LOCATION: (159)..(178)  
; OTHER INFORMATION: 2 (Potential)  
; NAME/KEY: DOMAIN  
; LOCATION: (179)..(203)  
; OTHER INFORMATION: Extracellular (Potential)  
; NAME/KEY: TRANSMEM  
; LOCATION: (204)..(227)  
; OTHER INFORMATION: 3 (Potential)  
; NAME/KEY: DOMAIN  
; LOCATION: (228)..(240)  
; OTHER INFORMATION: Cytoplasmic (Potential)  
; NAME/KEY: TRANSMEM  
; LOCATION: (241)..(262)  
; OTHER INFORMATION: 4 (Potential)  
; NAME/KEY: DOMAIN  
; LOCATION: (263)..(279)  
; OTHER INFORMATION: Extracellular (Potential)  
; NAME/KEY: TRANSMEM  
; LOCATION: (280)..(303)  
; OTHER INFORMATION: 5 (Potential)  
; NAME/KEY: DOMAIN  
; LOCATION: (304)..(328)  
; OTHER INFORMATION: Cytoplasmic (Potential)  
; NAME/KEY: TRANSMEM  
; LOCATION: (329)..(348)  
; OTHER INFORMATION: 6 (Potential)  
; NAME/KEY: DOMAIN  
; LOCATION: (349)..(360)  
; OTHER INFORMATION: Extracellular (Potential)

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; NAME/KEY: TRANSMEM
; LOCATION: (361)..(380)
; OTHER INFORMATION: 7 (Potential)
; NAME/KEY: DOMAIN
; LOCATION: (381)..(438)
; OTHER INFORMATION: Cytoplasmic (potential)
; NAME/KEY: CARBOHYD
; LOCATION: (58)..(58)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; NAME/KEY: CARBOHYD
; LOCATION: (88)..(88)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; NAME/KEY: CARBOHYD
; LOCATION: (92)..(92)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
US-09-983-000a-20

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Query Match      100.0%; Score 2342; DB 25; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120

QY 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLPRKHLCTRNTHLNLFLSFILRAISVLVKD 180
Db 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLPRKHLCTRNTHLNLFLSFILRAISVLVKD 180

QY 181 DVLSSSGTLCPCDPPSSWVGCKLSLVFQVCIMANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLSSSGTLCPCDPPSSWVGCKLSLVFQVCIMANFFWLLVEGLYHLTLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDTHDSVPMWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDTHDSVPMWVIRIPILISIIIVNFVLF 300

QY 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360
Db 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVQCELKRWRSRCPGPSASRDYRVCSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVAVLYCFNLSEVQCELKRWRSRCPGPSASRDYRVCSSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438
Db 421 FHRGSAQSFLQTETSVI 438

```

```

RESULT 6
US-10-273-573-8498
; Sequence 8498, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8498
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (133)..(179)
; OTHER INFORMATION: G-protein coupled receptors family 2 proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00649B, p-value=9.625e-
; OTHER INFORMATION: 38, raw score of 20.68
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (123)..(382)
; OTHER INFORMATION: 7 transmembrane receptor (Secretin family) domain identified
; OTHER INFORMATION: by Pfam, accession name 7tm_2, E-value=8.8e-131, Pfam score of
; OTHER INFORMATION: 447.9
US-10-273-573-8498

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Query Match      100.0%; Score 2342; DB 28; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECRPHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPEDESKI 120

QY 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLPRKHLCTRNTHLNLFLSFILRAISVLVKD 180
Db 121 TFYILVKAITYLGYSVLSLMSLATGSIILCLPRKHLCTRNTHLNLFLSFILRAISVLVKD 180

QY 181 DVLSSSGTLCPCDPPSSWVGCKLSLVFQVCIMANFFWLLVEGLYHLTLVAMLPERRC 240
Db 181 DVLSSSGTLCPCDPPSSWVGCKLSLVFQVCIMANFFWLLVEGLYHLTLVAMLPERRC 240

QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDTHDSVPMWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDTHDSVPMWVIRIPILISIIIVNFVLF 300

QY 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360
Db 301 SIIRILLOKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360

QY 361 LCLGSFQGLVAVLYCFNLSEVQCELKRWRSRCPGPSASRDYRVCSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVAVLYCFNLSEVQCELKRWRSRCPGPSASRDYRVCSSFSRNGSEGAQ 420

QY 421 FHRGSAQSFLQTETSVI 438
Db 421 FHRGSAQSFLQTETSVI 438

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RESULT 7
US-10-404-618-90
; Sequence 90, Application US/10404618
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare M.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Lora, Jose M.
; APPLICANT: White, David
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Robison, Keith E.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL 15571, 2465, 14266, 2882, 52871,
; TITLE OF INVENTION: 8203 AND 16852 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0530MNM
; CURRENT APPLICATION NUMBER: US/10/404,618
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/631,603
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781

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; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 09/794,763
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,942
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/634,392
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/176,075
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/013,634
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: 09/884,430
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/269,758
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-618-90

Query Match      100.0%; Score 2342; DB 30; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPCKRFHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPCKRFHLEIOEETKCAELLRSQTEKHKACSGVWDNIT 60

QY 61 CWRPANVGSTVTPCPKVSFNFYSKAGNISKNCTSDGWSFDPFVDACGYSDPEDESKI 120
Db 61 CWRPANVGSTVTPCPKVSFNFYSKAGNISKNCTSDGWSFDPFVDACGYSDPEDESKI 120

QY 121 TFYILVKALYTLGYSLSLMSLATGSIILCLFRKLHCTRNVIHNLFLSFILRAISVLVD 180
Db 121 TFYILVKALYTLGYSLSLMSLATGSIILCLFRKLHCTRNVIHNLFLSFILRAISVLVD 180

QY 181 DVLYSSTGLHCPDQPSWVGCKLSVFLQYCIIMANFFWLLVEGLYLHTLLVAMLPFPRC 240
Db 181 DVLYSSTGLHCPDQPSWVGCKLSVFLQYCIIMANFFWLLVEGLYLHTLLVAMLPFPRC 240

QY 241 FLAYLLIGHLPTVCIGAWTAARLYLEDTCWDNTDHSVPWWVIRIPILISIIIVNFVLF 300
Db 241 FLAYLLIGHLPTVCIGAWTAARLYLEDTCWDNTDHSVPWWVIRIPILISIIIVNFVLF 300

QY 301 SIIRILLOKLTSPDVGNDQSQVKRLAKSTLILLIPLFGVHYMVFAVFPISISKYQILPE 360
Db 301 SIIRILLOKLTSPDVGNDQSQVKRLAKSTLILLIPLFGVHYMVFAVFPISISKYQILPE 360

QY 361 LCLGSFQGLVAVLYLFLNSEVOCELKRWKRSRCPPTPSARDYRVCGSFSFRNGSEGLQ 420
Db 361 LCLGSFQGLVAVLYLFLNSEVOCELKRWKRSRCPPTPSARDYRVCGSFSFRNGSEGLQ 420

QY 421 FHRGSAQSFLOTETSVI 438
Db 421 FHRGSAQSFLOTETSVI 438

RESULT 8
US-10-652-981-20
; Sequence 20, Application US/10652981
; GENERAL INFORMATION:
; APPLICANT: AGY Therapeutics
; APPLICANT: Melcher, Thorsten
; APPLICANT: Mueller, Sabine
; APPLICANT: Chin, Daniel
; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZ
; TITLE OF INVENTION: OF BRAIN TUMORS
```

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; FILE REFERENCE: 263/180 -- PBagleman -- AGY
; CURRENT APPLICATION NUMBER: US/10/652,981
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/983,000A
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(23)
; OTHER INFORMATION: Potential
; FEATURE:
; NAME/KEY: GENE
; LOCATION: (1)..(438)
; OTHER INFORMATION: Vasoactive Intestinal Peptide Receptor 2
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (24)..(438)
; OTHER INFORMATION: Vasoactive Intestinal Polypeptide Receptor 2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)..(126)
; OTHER INFORMATION: 1 (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (127)..(151)
; OTHER INFORMATION: 1 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (152)..(158)
; OTHER INFORMATION: Cytoplasmic (potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (159)..(178)
; OTHER INFORMATION: 2 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (179)..(203)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (204)..(227)
; OTHER INFORMATION: 3 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (228)..(240)
; OTHER INFORMATION: Cytoplasmic (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (241)..(262)
; OTHER INFORMATION: 4 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (263)..(279)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (280)..(303)
; OTHER INFORMATION: 5 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (304)..(328)
; OTHER INFORMATION: Cytoplasmic (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (329)..(348)
; OTHER INFORMATION: 6 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
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; LOCATION: (349)..(360)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (361)..(380)
; OTHER INFORMATION: 7 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (381)..(438)
; OTHER INFORMATION: Cytoplasmic (potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (58)..(58)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (88)..(88)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (92)..(92)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; US-10-652-981-20

Query Match      100.0%; Score 2342; DB 31; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180

Qy 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAMLPERRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPIILSIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPIILSIIVNFVLF 300

Qy 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360

Qy 361 LCLGSFQGLVVAVLYCFLNSEVQCELKRWRSRPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFLNSEVQCELKRWRSRPTPSASRDYRVCGSSFSRNGSEGAQ 420

Qy 421 FHRGSRAGSFLQTETSVI 438
Db 421 FHRGSRAGSFLQTETSVI 438

RESULT 9
US-60-443-566-4403
; Sequence 4403, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102

; LOCATION: (349)..(360)
; OTHER INFORMATION: Extracellular (Potential)
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (361)..(380)
; OTHER INFORMATION: 7 (Potential)
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (381)..(438)
; OTHER INFORMATION: Cytoplasmic (potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (58)..(58)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (88)..(88)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (92)..(92)
; OTHER INFORMATION: N-linked (GLCNAC...) (Potential)
; US-10-652-981-20

Query Match      100.0%; Score 2342; DB 31; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180

Qy 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAMLPERRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPIILSIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPIILSIIVNFVLF 300

Qy 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360

Qy 361 LCLGSFQGLVVAVLYCFLNSEVQCELKRWRSRPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFLNSEVQCELKRWRSRPTPSASRDYRVCGSSFSRNGSEGAQ 420

Qy 421 FHRGSRAGSFLQTETSVI 438
Db 421 FHRGSRAGSFLQTETSVI 438

RESULT 9
US-60-443-566-4403
; Sequence 4403, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001447
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4403
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-443-566-4403

Query Match      100.0%; Score 2342; DB 33; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180
Db 121 TFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNHYIHLNLFILRAISVLVKD 180

Qy 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAMLPERRC 240
Db 181 DVLYSSGTLHCPDQPSWVGCKLSLVFLQYCI MANFFWLLVEGLYLHTLLVAMLPERRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPIILSIIVNFVLF 300
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPIILSIIVNFVLF 300

Qy 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360
Db 301 SIIRILLQKLTSPDVGNDQSYKRLAKSTLLIPLFGVHYMVFAVFPISISKYQILFE 360

Qy 361 LCLGSFQGLVVAVLYCFLNSEVQCELKRWRSRPTPSASRDYRVCGSSFSRNGSEGAQ 420
Db 361 LCLGSFQGLVVAVLYCFLNSEVQCELKRWRSRPTPSASRDYRVCGSSFSRNGSEGAQ 420

Qy 421 FHRGSRAGSFLQTETSVI 438
Db 421 FHRGSRAGSFLQTETSVI 438

RESULT 10
US-60-453-050-10294
; Sequence 10294, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10294
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-10294

Query Match      100.0%; Score 2342; DB 33; Length 438;
Best Local Similarity 100.0%; Pred. No. 1e-212;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60
Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIQEETKCAELLRSQTEKHKACSGWMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDPVDACGYSDPEDESKI 120

```

Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
 Qy 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLFILAISVLVKD 180  
 Db 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLFILAISVLVKD 180  
 Qy 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPFPRRC 240  
 Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPFPRRC 240  
 Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300  
 Db 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300  
 Qy 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360  
 Db 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360  
 Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
 Db 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
 Qy 421 FHRGSRQSFLOTETSVI 438  
 Db 421 FHRGSRQSFLOTETSVI 438

## RESULT 11

US-60-453-135-10294  
 ; Sequence 10294, Application US/60453135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: IAKOUBOVA, Olga  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001456  
 ; CURRENT APPLICATION NUMBER: US/60/453,135  
 ; CURRENT FILING DATE: 2003-03-10  
 ; NUMBER OF SEQ ID NOS: 82762  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10294  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-453-135-10294

Query Match 100.0%; Score 2342; DB 33; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-212;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60  
 Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
 Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLFILAISVLVKD 180  
 Db 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLFILAISVLVKD 180

Qy 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPFPRRC 240  
 Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPFPRRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300  
 Db 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300

Qy 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360  
 Db 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360

Qy 421 FHRGSRQSFLOTETSVI 438  
 Db 421 FHRGSRQSFLOTETSVI 438

## RESULT 13

US-60-465-241-5513  
 ; Sequence 5513, Application US/60465241  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: BEGOVICH, Ann  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
 Db 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
 Qy 421 FHRGSRQSFLOTETSVI 438  
 Db 421 FHRGSRQSFLOTETSVI 438

## RESULT 12

US-60-455-444-5513  
 ; Sequence 5513, Application US/60455444  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: BEGOVICH, Ann  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001455  
 ; CURRENT APPLICATION NUMBER: US/60/455,444  
 ; CURRENT FILING DATE: 2003-03-18  
 ; NUMBER OF SEQ ID NOS: 50986  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5513  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-455-444-5513

Query Match 100.0%; Score 2342; DB 33; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-212;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60  
 Db 1 MRTLPPALLTCWLLAPVNSIHPECFHLEIOEETKCAELLRSQTEKHKACSGVMDNIT 60

Qy 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120  
 Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGWSSETFPDFVDACGYSDPEDESKI 120

Qy 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLFILAISVLVKD 180  
 Db 121 TFYILVKAIYTLGYSVSLMSLATGSIILCLFRKLHCTRNYIHLNLFSLFILAISVLVKD 180

Qy 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPFPRRC 240  
 Db 181 DVLYSSSGTLHCPDQPSWVGCKLSLVFLQYICIMANFFWLLVEGLYHLLVAMLPFPRRC 240

Qy 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300  
 Db 241 FLAYLLIGWGLPTVCIGAWTAARLYEDTGCWDTNDHSPVWVIRIPILISIVNFVLF 300

Qy 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360  
 Db 301 SIIRILLOKLTSPDVGGNDQSKYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILPE 360

Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
 Db 361 LCLGSFQGLVAVLYCFNLSEVQCELCRKRWSRCPTPSASRDYRVCGSFSRNGSEGLQ 420

Qy 421 FHRGSRQSFLOTETSVI 438  
 Db 421 FHRGSRQSFLOTETSVI 438

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001468  
 ; CURRENT APPLICATION NUMBER: US/60/465,241  
 ; CURRENT FILING DATE: 2003-04-23  
 ; NUMBER OF SEQ ID NOS: 258418  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5513  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-465-241-5513

Query Match 100.0%; Score 2342; DB 33; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-212;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLIEQBEETKCAELLRSQTEKHKACSGWMDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHLIEQBEETKCAELLRSQTEKHKACSGWMDNIT 60  
 QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120  
 DB 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120  
 QY 121 TFYILVKAITYLGYSVLSMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGYSVLSMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
 QY 181 DVLYSSSGTLHCPDQPSWGWCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
 DB 181 DVLYSSSGTLHCPDQPSWGWCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
 QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
 QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360  
 QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 DB 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 QY 421 FHRGSAQSFIQTETSVI 438  
 DB 421 FHRGSAQSFIQTETSVI 438

RESULT 14  
 US-60-466-412-10294  
 ; Sequence 10294, Application US/60466412  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: IAKOUROVA, Olga  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001466  
 ; CURRENT APPLICATION NUMBER: US/60/466,412  
 ; CURRENT FILING DATE: 2003-04-30  
 ; NUMBER OF SEQ ID NOS: 429241  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10294  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-466-412-10294

Query Match 100.0%; Score 2342; DB 33; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-212;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLIEQBEETKCAELLRSQTEKHKACSGWMDNIT 60

DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHLIEQBEETKCAELLRSQTEKHKACSGWMDNIT 60  
 QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120  
 DB 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120  
 QY 121 TFYILVKAITYLGYSVLSMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGYSVLSMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
 QY 181 DVLYSSSGTLHCPDQPSWGWCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
 DB 181 DVLYSSSGTLHCPDQPSWGWCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
 QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
 DB 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300  
 QY 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360  
 DB 301 SIIRILLOKLTSPDVGGNDQSOYKRLAKSTLLIPLFGVHYMFAVFPISISSKYQILFE 360  
 QY 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 DB 361 LCLGSFQGLVVAVLYCFLNSEVQCELRKWRSCPTPSASRDYRVCGSSFSRNGSEGALQ 420  
 QY 421 FHRGSAQSFIQTETSVI 438  
 DB 421 FHRGSAQSFIQTETSVI 438

## RESULT 15

US-60-500-315-1460  
 ; Sequence 1460, Application US/60500315  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
 ; TITLE OF INVENTION: ENCODING HUMAN G-PROTEIN COUPLED RECEPTOR PROTEINS, METHODS  
 ; TITLE OF INVENTION: OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001484  
 ; CURRENT APPLICATION NUMBER: US/60/500,315  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 69978  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1460  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-500-315-1460

Query Match 100.0%; Score 2342; DB 33; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 1e-212;  
 Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLIEQBEETKCAELLRSQTEKHKACSGWMDNIT 60  
 DB 1 MRTLPPALLTCWLLAPVNSIHPECRFHLIEQBEETKCAELLRSQTEKHKACSGWMDNIT 60  
 QY 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120  
 DB 61 CWRPANVGETVTVPCKVFSNFYSKAGNISKNCTSDGWSSETFPDFVDACGSDPEDSKI 120  
 QY 121 TFYILVKAITYLGYSVLSMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
 DB 121 TFYILVKAITYLGYSVLSMSLATGSIILCLFRKLHCTRNVIHLNLFILRAISVLVKD 180  
 QY 181 DVLYSSSGTLHCPDQPSWGWCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
 DB 181 DVLYSSSGTLHCPDQPSWGWCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
 QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVPMWVIRIPILISIIIVNVLFI 300

Db 241 FLAYLLIGWLEPTVCIGAWTAARLYLEDTGCDTNDHSVPWWVIRIPILISIIIVNFVLEI 300  
Qy 301 SIIRILLOKLTSPDVGGNDQSOYKRIAKSTLLIIPFGVHYMVFAVFPISISSKYQIILFE 360  
Db 301 SIIRILLOKLTSPDVGGNDQSOYKRIAKSTLLIIPFGVHYMVFAVFPISISSKYQIILFE 360  
Qy 361 LCLGSFQGLVAVLYCFNLSEVQCELKKWRRCPTPSASRDYRVCGSSFSGSEGALQ 420  
Db 361 LCLGSFQGLVAVLYCFNLSEVQCELKKWRRCPTPSASRDYRVCGSSFSGSEGALQ 420  
Qy 421 FHRGSAQSFLQETSTVI 438  
Db 421 FHRGSAQSFLQETSTVI 438

Search completed: June 22, 2004, 09:03:25  
Job time : 185 secs



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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:58:09 ; Search time 21 seconds

(without alignments)  
950.959 Million cell updates/sec

Title: US-09-983-000A-20

Perfect score: 2342

Sequence: 1 MRTLPPALLTCWLLAPVNS.....LQFHGRSAQSFLOTETSVI 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 302192 seqs, 45593913 residues

Total number of hits satisfying chosen parameters: 302192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA New:\*

- 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*
- 7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2342	100.0	438	6	US-10-831-393-10
2	2331	99.5	438	6	US-10-831-393-12
3	2327	99.4	438	6	US-10-831-393-11
4	2032	86.8	437	6	US-10-831-393-14
5	2032	86.8	437	6	US-10-831-393-16
6	2030	86.7	437	6	US-10-831-393-13
7	2020	86.3	437	6	US-10-831-393-15
8	1141.5	48.7	444	6	US-10-831-393-6
9	1086	46.5	459	6	US-10-831-393-4
10	1064.5	45.5	459	6	US-10-831-393-3
11	1064.5	45.5	459	6	US-10-831-393-8
12	1059	45.2	458	6	US-10-831-393-5
13	1059	45.2	458	6	US-10-831-393-7
14	1035.5	44.2	457	6	US-10-831-393-1
15	1035.5	44.2	457	7	US-60-568-073-1217
16	1026	43.8	447	6	US-10-831-393-9
17	1024	43.7	460	6	US-10-831-393-2
18	914.5	39.0	404	1	PCT-US04-09049-1
19	669	28.6	466	6	US-10-775-204-2219
20	669	28.6	466	6	US-10-796-307-662
21	669	28.5	466	7	US-60-550-051-292
22	644.5	27.5	419	6	US-10-796-307-663
23	644.5	27.5	419	7	US-60-550-051-293
24	564	24.1	443	1	PCT-US04-09049-10
25	486	20.8	411	6	US-10-821-502-8
26	483	20.6	431	6	US-10-821-502-2

27	482	20.6	411	6	US-10-821-502-4	Sequence 4, Appli
28	459.5	19.6	241	1	PCT-US04-09049-2	Sequence 2, Appli
29	451.5	19.3	504	6	US-10-489-425-32	Sequence 32, Appl
30	441.5	18.9	463	6	US-10-490-594-14	Sequence 14, Appl
31	434.5	18.6	464	6	US-10-490-594-12	Sequence 12, Appl
32	428.5	18.3	461	6	US-10-489-425-30	Sequence 10, Appl
33	424.5	18.1	431	6	US-10-489-425-30	Sequence 30, Appl
34	403.5	17.2	395	6	US-10-489-425-108	Sequence 108, App
35	224	9.6	618	6	US-10-473-391-7	Sequence 7, Appli
36	222	9.5	785	6	US-10-821-234-1164	Sequence 1164, Ap
37	222	9.5	835	1	PCT-US03-15011-56	Sequence 56, Appl
38	222	9.5	835	1	PCT-US03-15011-57	Sequence 57, Appl
39	219	9.4	823	1	PCT-US03-15011-44	Sequence 44, Appl
40	219	9.4	823	1	PCT-US03-15011-62	Sequence 62, Appl
41	217.5	9.3	872	1	PCT-US03-15011-66	Sequence 66, Appl
42	213.5	9.1	741	6	US-10-667-762-40	Sequence 40, Appl
43	210.5	9.0	344	1	PCT-US03-15011-63	Sequence 63, Appl
44	207	8.8	652	1	PCT-US03-15011-65	Sequence 65, Appl
45	207	8.8	652	6	US-10-667-762-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-831-393-10  
; Sequence 10, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US/09/694,519  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: homo sapiens;  
US-10-831-393-10

Query Match	100.0%;	Score 2342;	DB 6;	Length 438;
Best Local Similarity	100.0%;	Pred. No. 1.1e-193;		
Matches	438;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MRTLPPALLTCWLLAPVNSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGWONIT	60	
Db	1	MRTLPPALLTCWLLAPVNSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGWONIT	60	
Qy	61	CWRPNYGETVTPCPKVFNFYSKAGNISKNCTSDGWSSTFFDFVACGYSDPEDESKI	120	
Db	61	CWRPNYGETVTPCPKVFNFYSKAGNISKNCTSDGWSSTFFDFVACGYSDPEDESKI	120	
Qy	121	TFYLKVAIYTLGVSVLSLMSLATGSIILCLFRKLCHTRNYTHNLFLSFILRAISVLVD	180	
Db	121	TFYLKVAIYTLGVSVLSLMSLATGSIILCLFRKLCHTRNYTHNLFLSFILRAISVLVD	180	
Qy	181	DVLYSSGTLHCPDQSSSWGCKLSLVFLOYCIMANFFWLLVEGLYHTLLVAMLPERRC	240	
Db	181	DVLYSSGTLHCPDQSSSWGCKLSLVFLOYCIMANFFWLLVEGLYHTLLVAMLPERRC	240	
Qy	241	FLAYLLIGWGLPTVCIGAWTAARLYEDTCGWDNTHSVPMWVIRIPILISIIWNFVLF	300	
Db	241	FLAYLLIGWGLPTVCIGAWTAARLYEDTCGWDNTHSVPMWVIRIPILISIIWNFVLF	300	
Qy	301	SIIRILLOKLTSPDVGNDOSQYKRLAKSTLLIPLFGVHYMVFAPVPISSKYQILFE	360	
Db	301	SIIRILLOKLTSPDVGNDOSQYKRLAKSTLLIPLFGVHYMVFAPVPISSKYQILFE	360	

QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
Db 361 LCLGSFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
QY 421 FHRGSAQSFLOTETSVI 438  
Db 421 FHRGSAQSFLOTETSVI 438

## RESULT 2

US-10-831-393-12  
; Sequence 12, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; PRIOR APPLICATION NUMBER: 2004-04-23  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 12  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-831-393-12

Query Match 99.5%; Score 2331; DB 6; Length 438;  
Best Local Similarity 99.5%; Pred. No. 9.6e-193;  
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPDESKI 120  
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPDESKI 120  
QY 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180  
Db 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180  
QY 181 DVLVSSSGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
Db 181 DVLVSSSGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIIVNVLFI 300  
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIIVNVLFI 300  
QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
Db 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
Db 361 LCLGSFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
QY 421 FHRGSAQSFLOTETSVI 438  
Db 421 FHRGSAQSFLOTETSVI 438

## RESULT 3

US-10-831-393-11  
; Sequence 11, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell

; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; PRIOR APPLICATION NUMBER: 2004-04-23  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 11  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: homo sapiens;  
US-10-831-393-11

Query Match 99.4%; Score 2327; DB 6; Length 438;  
Best Local Similarity 99.3%; Pred. No. 2.1e-192;  
Matches 435; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
Db 1 MRTLPPALLTCWLLAPVNSIHPECRFHLEIQEETKCAELRSQTEKHKACSGVWDNIT 60  
QY 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPDESKI 120  
Db 61 CWRPANVGETVTPCPKVFNSFYKAGNISKNCTSDGMSSETFPDFVDACGYSDPDESKI 120  
QY 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180  
Db 121 TFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSLRAISVLVKD 180  
QY 181 DVLVSSSGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
Db 181 DVLVSSSGTLHCPDPSSWVGCKLSLVFLQYCI MANFFWLLVEGLYHLTLVAMLPERRC 240  
QY 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIIVNVLFI 300  
Db 241 FLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSDVPMWVIRIPILISIIIVNVLFI 300  
QY 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
Db 301 SIIRILLQKLTSPDVGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPISISSKYQILFE 360  
QY 361 LCLGSFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
Db 361 LCLGSFQGLVAVLYCFLNSEVQCELRKRWRCPTPSASRDYRVCGSFSRNGSEGLQ 420  
QY 421 FHRGSAQSFLOTETSVI 438  
Db 421 FHRGSAQSFLOTETSVI 438

## RESULT 4

US-10-831-393-14  
; Sequence 14, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; PRIOR APPLICATION NUMBER: 2004-04-23  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 14  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: rattus norvegicus;  
US-10-831-393-14

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Query Match      86.8%; Score 2032; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 5e-167;
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

Qy 12 CWWLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWWLVRVSSIHPECRFHEIQEETKCAELLSSQWENHRACSGVMDNITCWRPADIGTV 70

Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVADACGYSDPDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPDESKITFYILVKAITY 130

Qy 132 LGYSVSLMSLTGSIILCLFRKLHCTRNYIHLNLFSLFMRALSVLVKDVLYSSSGTLH 191
Db 131 LGYSVSLMSLTGSIILCLFRKLHCTRNYIHLNLFSLFMRALSVLVKDVLYSSSGTLR 190

Qy 192 CPDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAMLPFRCFLAYLLIGWGL 251
Db 191 CHDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAILPPSRCLFAYLLIGWGI 250

Qy 252 PTVCIGAWTAARLYLEDTGCDWTDNDHSVPWWVIRIPILISIVNVFVLFISIRILLQKLT 311
Db 251 PSVCIGAWIATRLSLEDTGCDWTDNDHSIPWWVIRMPILISIVNVFALFISIRILLQKLT 310

Qy 312 SPDVGGNDQSQYKRLAKSTLLIPFGVHYVMVFAVFPISISSKYQIILFELCLGSFQGLV 371
Db 311 SPDVGGNDQSQYKRLAKSTLLIPFGVHYVMVFAVFPISISSKYQIILFELCLGSFQGLV 370

Qy 372 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSSFSRNGSEGLAQHGRSRAOSFL 431
Db 371 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSSFSRNGSEGLAQHGRSRTOSFL 430

Qy 432 QTETSVI 438
Db 431 QSETSVI 437

RESULT 5
US-10-831-393-16
; Sequence 16, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or H
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 437
; TYPE: PRT
; ORGANISM: rat;
US-10-831-393-16

Query Match      86.8%; Score 2032; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 5e-167;
Matches 373; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

Qy 12 CWWLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWWLVRVSSIHPECRFHEIQEETKCAELLSSQWENHRACSGVMDNITCWRPADIGTV 70

Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVADACGYSDPDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPDESKITFYILVKAITY 130

Qy 132 LGYSVSLMSLTGSIILCLFRKLHCTRNYIHLNLFSLFMRALSVLVKDVLYSSSGTLH 191
Db 131 LGYSVSLMSLTGSIILCLFRKLHCTRNYIHLNLFSLFMRALSVLVKDVLYSSSGTLR 190
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Qy 192 CPDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAMLPFRCFLAYLLIGWGL 251
Db 191 CHDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAILPPSRCLFAYLLIGWGI 250

Qy 252 PTVCIGAWTAARLYLEDTGCDWTDNDHSVPWWVIRIPILISIVNVFVLFISIRILLQKLT 311
Db 251 PSVCIGAWIATRLSLEDTGCDWTDNDHSIPWWVIRMPILISIVNVFALFISIRILLQKLT 310

Qy 312 SPDVGGNDQSQYKRLAKSTLLIPFGVHYVMVFAVFPISISSKYQIILFELCLGSFQGLV 371
Db 311 SPDVGGNDQSQYKRLAKSTLLIPFGVHYVMVFAVFPISISSKYQIILFELCLGSFQGLV 370

Qy 372 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSSFSRNGSEGLAQHGRSRAOSFL 431
Db 371 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSSFSRNGSEGLAQHGRSRTOSFL 430

Qy 432 QTETSVI 438
Db 431 QSETSVI 437

RESULT 6
US-10-831-393-13
; Sequence 13, Application US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or I
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: mus musculus;
US-10-831-393-13

Query Match      86.7%; Score 2030; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 7.5e-167;
Matches 373; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

Qy 12 CWWLAPVNSIHPECRFHEIQEETKCAELLRSQTEKHKACSGVMDNITCWRPANVGTV 71
Db 11 CWWLVRVSSIHPECRFHEIQEETKCAELLSSQWENHRACSGVMDNITCWRPADVGTV 70

Qy 72 TVPCPKVFSNFYSKAGNISKNCTSDGWSSETFPDFVADACGYSDPDESKITFYILVKAITY 131
Db 71 TVPCPKVFSNFYSRPGNISKNCTSDGWSSETFPDFIDACGYNDPDESKISFYILVKAITY 130

Qy 132 LGYSVSLMSLTGSIILCLFRKLHCTRNYIHLNLFSLFMRALSVLVKDVLYSSSGTLH 191
Db 131 LGYSVSLMSLTGSIILCLFRKLHCTRNYIHLNLFSLFMRALSVLVKDVLYSSSGTLR 190

Qy 192 CPDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAMLPFRCFLAYLLIGWGL 251
Db 191 CHDQPSWVGCKLSLVFQYICIMANFWLLVEGLYHTLLVAILPPSRCLFAYLLIGWGI 250

Qy 252 PTVCIGAWTAARLYLEDTGCDWTDNDHSVPWWVIRIPILISIVNVFVLFISIRILLQKLT 311
Db 251 PSVCIGAWIATRLSLEDTGCDWTDNDHSIPWWVIRMPILISIVNVFALFISIRILLQKLT 310

Qy 312 SPDVGGNDQSQYKRLAKSTLLIPFGVHYVMVFAVFPISISSKYQIILFELCLGSFQGLV 371
Db 311 SPDVGGNDQSQYKRLAKSTLLIPFGVHYVMVFAVFPISISSKYQIILFELCLGSFQGLV 370

Qy 372 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSSFSRNGSEGLAQHGRSRAOSFL 431
Db 371 AVLYCFNLSEVQCELKRWKRCPTPSASRDYRVCGSSFSRNGSEGLAQHGRSRTOSFL 430
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Db 371 AVLYCFNLSEVOCELKRRWRGLCLTQAGSRDYHLHWSMSRNGSESGALQIHRGSRQSF 430  
QY 432 QETSVI 438  
Db 431 QETSVI 437

## RESULT 7

US-10-831-393-15  
; Sequence 15, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US/09/694,519  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: rattus norvegicus;  
US-10-831-393-15

Query Match 86.3%; Score 2020; DB 6; Length 437;  
Best Local Similarity 87.1%; Pred. No. 5.4e-166;  
Matches 372; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 12 CWLLAPVNSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGVNDITCWPANVETV 71  
Db 11 CWLLVRVSSIHPECRPHLEIQBEETKCAELLRSQTEKHKACSGVNDITCWPADIGETV 70  
QY 72 TVPCPKVFSNFYSKAGNISKNCTSDGSETFPD FVDACGSDPEDESKITFYILVKAIYT 131  
Db 71 TVPCPKVFSNFYSRPNISKNCTSDGSETFPD FIDACGYNDPEDESKITFYILVKAIYT 130  
QY 132 LGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSFILRAISVLKDDVLYSSGTLH 191  
Db 131 LGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSFILRAISVLKDDVLYSSGTLR 190  
QY 192 CPDQPSWVGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLP RRCFLAYLLIGWGL 251  
Db 191 CHDQGSWVGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLVAMLP RRCFLAYLLIGWGI 250  
QY 252 PVVICGAWTAARLYLEDTCGWDNDHNSVPMWVIRIPILISIVNFVLFISIRILLQKIT 311  
Db 251 PSVCIGAWTATLSLEDTCGWDNDHNSIPMWVIRIPILISIVNFVLFISIRILLQKIT 310  
QY 312 SPDVGNDQSOYKRLAKSTLLILPLFGVHYMVFAVFPISISKYQLLFCGLGSGQLV 371  
Db 311 SPDVGNDQSOYKRLAKSTLLILPLFGVHYMVFAVFPISISKYQLLFCGLGSGQLV 370  
QY 372 AVLYCFNLSEVOCELKRRWRSCPTPSASRDYRVCGSFRNGSESGALQIHRGSRQSF 431  
Db 371 AVLYCFNLSEVOCELKRRWRGLCLTQAGSRDYHLHWSMSRNGSESGALQIHRGSRQSF 430  
QY 432 QETSVI 438  
Db 431 QETSVI 437

## RESULT 8

US-10-831-393-6  
; Sequence 6, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors

; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US/09/694,519  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: rana ridibunda;  
US-10-831-393-6

Query Match 48.7%; Score 1141.5; DB 6; Length 444;  
Best Local Similarity 51.9%; Pred. No. 2e-90;  
Matches 233; Conservative 65; Mismatches 128; Indels 23; Gaps 10;

QY 5 LPPALLTCWLLAPVNSIHPEC--RPHLEIQBEETKCAELLRSQTEKHKACSGVNDITC 62  
Db 4 LPLLCLCLTGLSPILCVPECSIMYQIELKHEECVNHEDYFNDT---AVCKRTWNDITCW 60  
QY 63 RPAVGETVTVPCPKVFSNFYSKA--GNISKNCTSDGSETFP--DFVDACGYS--DPDE 117  
Db 61 PSASIGEVVVLQCPGYFSMFTTGTGVNGVSNKCTSEGSEMYPATYAAACGFSNDTPT 120  
QY 118 SKITFYILVKAIYTLGYSVLSMLATGSIILCLFRKLHCTRYNIHLNPLSFILRAISVL 177  
Db 121 QQTVEFGAIGTYTIGHLSLSLTAAMLIILCIPFKLHCTRYNIHMLFMSFIMRAIAVF 180  
QY 178 VKDDVLYSSGTLHCPDQPSWVGCKLSLVFLOYCIMANFFWLLVEGLYLHTLLV-AMLP 236  
Db 181 LKDIVLFSGESDHC---HVGSVGCAAMVFOYICIMANFFWLLVEGLYLHNLVLSFSS 237  
QY 237 PRRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHNSVPMWVIRIPILISIVNF 296  
Db 238 EKXIFWVILIGWGAAPSVFITAWSLARVYFEDTGCWDTIESHL-WIIKTPLVLSILVNF 296  
QY 297 VLFISIRILLQKITSPDVGNDQSOYKRLAKSTLLILPLFGVHYMVFAVFPISISKYQ 356  
Db 297 LIFCIIIRILVQKLHSPDVGNENSQYTRLAKSTLLILPLFGVHYMFAFPDNPKEVK 356  
QY 357 ILFELCLSGPGLVAVLYCFNLSEVOCELKRRWRSCPTPSASRDYRVCGSFRNGSE 416  
Db 357 LVFELILGSGFGVAVLYCFNLSEVOCELKRRWRNLERFMGKMKYVHHPHSLGSGN 416  
QY 417 GALQPH-----RGSRAQSFIQETSVI 438  
Db 417 FSTQISMLTKCSPKTRRCSSF-QAEFSILV 444

## RESULT 9

US-10-831-393-4  
; Sequence 4, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831,393  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US/09/694,519  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: mus musculus;  
US-10-831-393-4

Query Match 46.4%; Score 1086; DB 6; Length 459;  
Best Local Similarity 48.5%; Pred. No. 1.3e-85;

Matches 225; Conservative 67; Mismatches 132; Indels 40; Gaps 11;

Qy 5 LPPALLTCWL-----LAPVN-----SHPECRPHLEIQTBEETKCAELLSQTE-KHKAC 52  
Db 6 LPPARWLVLGALACALGPAGSRAAPHOCEYLQMIKORQOCLE--EAQLENKTTGC 63  
Qy 53 SGWWDNITCWRPANVGETVTPCPKVFNSFYKAG-NISKNTSDGMSSTFP-DFVDACG 110  
Db 64 SKMWDNLTCWFTTPWGQVVDLDCPLIFQFSPHGYNISRNCTEAGSOLQEPGPHYLAOG 123  
Qy 111 YSD-----PEDESKITFYILVKAITYLGYSVLSMISLATSIIILCLPRKHLCTRNVIHNLFP 166  
Db 124 LNDRASSMDEQOQTEFYDAVKTGTIGYSLASLLVAMAILSLFRKLHCTRNVIHNLFP 183  
Qy 167 LSFILRAISVLVKDDVLYSSGTLHCPDQPSWGWCKLSLVFLQYCIANFFWLLVGLY 226  
Db 184 MSFILRATAVFIKQMAFNGETDHCSE---ASVCKAAVVFQYCVMANFFWLLVGLY 240  
Qy 227 LHTLL-VAMLPFRRCFLAYLLIGMGLTVCIGAWTAARLYLEDTCGWDTHDHSVPMWVIR 285  
Db 241 LHTLAVSFFSERKVFYWGVIILGWGVSFVIMTIWIRIHFEDFGCWDTHINSSLMWIK 300  
Qy 286 IPIILISIVNFVLSIRILLQKLTSPDVCGNDQSKYKRLAKSTLLIPLFGVHYWVFA 345  
Db 301 GPILISILVNFILFICIRILVQKLRPPDIGNKNDSSPYSLAKSTLLIPLFGVHYWVFA 360  
Qy 346 VFPISISSKYQILFELCLGSGFQGLVAVLYCFINSEVOCELKRWK-----SRC 394  
Db 361 FFPDNFAQKQVNFVVGSGFQGVVAILYCFNGEVQAEVLSV 459  
Qy 395 PTPSASRDYRVCSSFRNGSEGLQFHRGSAQSFLOTETSVI 438  
Db 421 QHPWGGSGNGVSCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 459

RESULT 10  
US-10-831-393-3  
; Sequence 3, Application US/10831393  
; GENERAL INFORMATION:  
; APPLICANT: Isfort, Robert  
; APPLICANT: Sheldon, Russell  
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F  
; FILE REFERENCE: 8311  
; CURRENT APPLICATION NUMBER: US/10/831.393  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: rattus norvegicus;  
US-10-831-393-3

Query Match 45.5%; Score 1064.5; DB 6; Length 459;  
Best Local Similarity 47.1%; Pred. No. 8.9e-84;  
Matches 221; Conservative 68; Mismatches 139; Indels 41; Gaps 11;

Qy 1 MRTLPP-----ALLTCWLLAPVN-----SHPECRPHLEIQTBEETKCAELLSQTE 47  
Db 1 MRPPSPPHVRLCWLALGALAC-ALRPAGSQAASPHQCEYLQLEIQRQOCLEBAQLENE 59  
Qy 48 KHKACSGWWDNITCWRPANVGETVTPCPKVFNSFYKAG-NISKNTSDGMSSTFP-DF 105  
Db 60 T-TGCSKMDNLTCWFTTPRQAVVLDCLPLIFQFAPIHGYNISRSCTEGWSQLEPGY 118  
Qy 106 VDAGYSDP-----BDESKITFYILVKAITYLGYSVLSMISLATSIIILCLPRKHLCTRNVI 161  
Db 119 HIACGLNDRASSLDEQOQTEFYNTVKTGTIGYSLASLLVAMAILSLFRKLHCTRNVI 178  
Qy 162 HLNLFLFILRAISVLVKDDVLYSSGTLHCPDQPSWGWCKLSLVFLQYCIANFFWLL 221  
Db 179 HMLFMSFILRATAVFIKQMAFNGETDHCSE---ASVCKAAVVFQYCVMANFFWLL 235  
Qy 222 VEGLYLHTLL-VAMLPFRRCFLAYLLIGMGLTVCIGAWTAARLYLEDTCGWDTHDHSV 280  
Db 236 VEGLYLHTLLAVSFFSERKVFYWGVIILGWGVSFVIMTIWIRIHFEDFGCWDTHINSS 295  
Qy 281 WWIRIPILISIVNFVLSIRILLQKLTSPDVCGNDQSKYKRLAKSTLLIPLFGVH 340  
Db 296 WWIIPKAPILISIVNFVLSIRILLQKLTSPDVCGNDQSKYKRLAKSTLLIPLFGVH 355  
Qy 341 YMFVAVFPISSISKYQILFELCLGSGFQGLVAVLYCFINSEVOCELKRWK----- 391  
Db 356 YMFVAFPPDNFAQKQVNFVVGSGFQGVVAILYCFNGEVQAEVLSV 459

Query Match 45.5%; Score 1064.5; DB 6; Length 459;  
Best Local Similarity 47.1%; Pred. No. 8.9e-84;  
Matches 221; Conservative 68; Mismatches 139; Indels 41; Gaps 11;

Qy 1 MRTLPP-----ALLTCWLLAPVN-----SHPECRPHLEIQTBEETKCAELLSQTE 47  
Db 1 MRPPSPPHVRLCWLALGALAC-ALRPAGSQAASPHQCEYLQLEIQRQOCLEBAQLENE 59  
Qy 48 KHKACSGWWDNITCWRPANVGETVTPCPKVFNSFYKAG-NISKNTSDGMSSTFP-DF 105  
Db 60 T-TGCSKMDNLTCWFTTPRQAVVLDCLPLIFQFAPIHGYNISRSCTEGWSQLEPGY 118  
Qy 106 VDAGYSDP-----BDESKITFYILVKAITYLGYSVLSMISLATSIIILCLPRKHLCTRNVI 161  
Db 119 HIACGLNDRASSLDEQOQTEFYNTVKTGTIGYSLASLLVAMAILSLFRKLHCTRNVI 178  
Qy 162 HLNLFLFILRAISVLVKDDVLYSSGTLHCPDQPSWGWCKLSLVFLQYCIANFFWLL 221

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392 --SRCPTPSASRDYRVCGSSFSRNGSEGAQFHRGSAQSFLOTETSVI 438
416 WSKSQHPWGGSGATCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 459

RESULT 12
US-10-831-393-5
; SEQUENCE 5, APPLICATION US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 458
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-831-393-5

Query Match 45.2%; Score 1059; DB 6; Length 458;
Best Local Similarity 46.9%; Pred. No. 2.7e-83;
Matches 220; Conservative 65; Mismatches 142; Indels 42; Gaps 12;

QY 1 MRTLPP-----ALLTCWLLAPVNS-----IHPCRFLHEIQEETKCAELRSQT 46
Db 1 MRPLSPPPAGWFCVLAVLAC-VLGPVGSWAVGLQOECDYLMIKVQHKKCLEEAQLEN 59
QY 47 EKHKACSGVNDNITCWRPANVGETVTPCPKVSFNYSKAG-NISKNCISDGHSETFP-D 104
Db 60 ET-SGCSKXNDNITCWRPANVGETVTPCPKVSFNYSKAG-NISKNCISDGHSETFP-D 118
QY 105 FVDACGYSDE---DESKITFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNYI 161
Db 119 YPIACGMDDKASGLDEQOTVFYNSVKTGYTIGVSLAALLVATAILSLFRKLHCTRNYI 178
QY 162 HMLFISFILRAISLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVPLQYICIMANFWLL 221
Db 179 HMLFISFILRAISLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVPLQYICIMANFWLL 235
QY 222 VEGLYLHTLL-VAMLPERRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVP 280
Db 236 VEGLYLHTLLAVSFSEKRYFWGYIFVGVGVSTFIMVTVRIHEDYGCWDT-IHSSL 294
QY 281 WVIPIILISIVNFWLFIIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVH 340
Db 295 WVIKAPILASILVNFILFIRIIGILVQKLRPPDVGKSDNSPYSRLAKSTLLIPLFGVH 354
QY 341 YMVFAVPPISISKYQLFELCLGSGFGLVAVLYCFLNSEVOCELKRWK 391
Db 355 YMFAPFPNFKAEVKKVFEIIVGSGCVVAILYCFNGEVOAELRRKRWKHHQGVLG 414
QY 392 --SRCPTPSASRDYRVCGSSFSRNGSEGAQFHRGSAQSFLOTETSVI 438
Db 415 WDSKYHPGGSGNGDTCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 458

RESULT 13
US-10-831-393-7
; SEQUENCE 7, APPLICATION US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
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; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 458
; TYPE: PRT
; ORGANISM: porcine
US-10-831-393-7

Query Match 45.2%; Score 1059; DB 6; Length 458;
Best Local Similarity 46.9%; Pred. No. 2.7e-83;
Matches 220; Conservative 65; Mismatches 142; Indels 42; Gaps 12;

QY 1 MRTLPP-----ALLTCWLLAPVNS-----IHPCRFLHEIQEETKCAELRSQT 46
Db 1 MRPLSPPPAGWFCVLAVLAC-VLGPVGSWAVGLQOECDYLMIKVQHKKCLEEAQLEN 59
QY 47 EKHKACSGVNDNITCWRPANVGETVTPCPKVSFNYSKAG-NISKNCISDGHSETFP-D 104
Db 60 ET-SGCSKXNDNITCWRPANVGETVTPCPKVSFNYSKAG-NISKNCISDGHSETFP-D 118
QY 105 FVDACGYSDE---DESKITFYILVKAIYTLGYSVLSMSLATGSIILCLFRKLHCTRNYI 161
Db 119 YPIACGMDDKASGLDEQOTVFYNSVKTGYTIGVSLAALLVATAILSLFRKLHCTRNYI 178
QY 162 HMLFISFILRAISLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVPLQYICIMANFWLL 221
Db 179 HMLFISFILRAISLVKDDVLYSSSGTLHCPDQPSWVGCKLSLVPLQYICIMANFWLL 235
QY 222 VEGLYLHTLL-VAMLPERRCFLAYLLIGWGLPTVCIGAWTAARLYLEDTCGWDNDHSVP 280
Db 236 VEGLYLHTLLAVSFSEKRYFWGYIFVGVGVSTFIMVTVRIHEDYGCWDT-IHSSL 294
QY 281 WVIPIILISIVNFWLFIIRILLOKLTSPDVGNDQSOYKRLAKSTLLIPLFGVH 340
Db 295 WVIKAPILASILVNFILFIRIIGILVQKLRPPDVGKSDNSPYSRLAKSTLLIPLFGVH 354
QY 341 YMVFAVPPISISKYQLFELCLGSGFGLVAVLYCFLNSEVOCELKRWK 391
Db 355 YMFAPFPNFKAEVKKVFEIIVGSGCVVAILYCFNGEVOAELRRKRWKHHQGVLG 414
QY 392 --SRCPTPSASRDYRVCGSSFSRNGSEGAQFHRGSAQSFLOTETSVI 438
Db 415 WDSKYHPGGSGNGDTCSTQVSM-----LTRVSPSARRSSSFQAEVSLV 458

RESULT 14
US-10-831-393-1
; SEQUENCE 1, APPLICATION US/10831393
; GENERAL INFORMATION:
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or F
; TITLE OF INVENTION: Using Vasoactive Intestinal Peptide Receptors
; FILE REFERENCE: 8311
; CURRENT APPLICATION NUMBER: US/10/831,393
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US/09/694,519
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 457
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-831-393-1

Query Match 44.2%; Score 1035.5; DB 6; Length 457;
Best Local Similarity 46.3%; Pred. No. 2.8e-81;
Matches 216; Conservative 68; Mismatches 144; Indels 39; Gaps 12;
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QY 1 MRTLTP-PALLTC-----WLLAPVNS-----IHPECRFHLEIOBEETKCAELLRSTQEX 48
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QY 49 HKACSGWMDNITCWRPANVGETVTPCPKVPNSFYKAG-NISKNTSDGMSFTFP-DFV 106
Db 61 -IGCSKMDNITCWPATPRGQVWVLAACPLIFKLFSSIQGRNVRSCTDEGWTLEPGYP 119
QY 107 DACGYSDEPE---DESKITFYILVKAITYLGVSVLSMSLATGSIILCLFRKLHCTRYIHL 163
Db 120 IACGLDDKAASLDEQQTWTFYGSVKTGYTIGVGLSLATLLVATALLSLFRKLHCTRYIHM 179
QY 164 NLFLSFILRAISVLVKDDVLYSSSTLHCPDPQSPSWGCKLSLVFLQYCI MANFFWLLVE 223
Db 180 HLFISFILRAAAVFIKDALFDSGESDQCE---GSVCKAAWVFFQYCVMANFFWLLVE 236
QY 224 GLYLHTLL-VAMLPERRCFLAYLIGWGLPTVCIGAMTAARLYLEDTCGWDNDHSPVW 282
Db 237 GLYLHTLLAVSFYFERRKYFWGYIILIGWGPSTFTMVWVTIARIHFEDYGCWDTINSSL-WW 295
QY 283 VIRIPILISIIIVNFVLFISIIRILLOKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYM 342
Db 296 IIKGPILTSILVNFILFICIIRILLOKLRPPDIRKSDSPYSRLARSTLLIPLFGVHYI 355
QY 343 VFVFPISISKYQILFELCLGSPQGLVAVLYCFLNSEVQCELRKWR----- 391
Db 356 MFAPFPDNFXDEKVMFELVVGSGFQGVVAILYCFLNGEVQAEELRRKWRWHLQGVLGWN 415
QY 392 SRCPTPSASRDYRVCGSFSRNGSEGAQPHRGSRASQFLQETSVI 438
Db 416 PKYRHPGGSGNGATCSTQVSM-----LTRVSPGARRSSSFQAEVSLV 457
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## RESULT 15

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US-60-568-073-1217
; Sequence 1217, Application US/60568073
; GENERAL INFORMATION:
; APPLICANT: Huang, Fei
; APPLICANT: Han, Xia
; APPLICANT: Shaw, Peter
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: COLON CANCER BIOMARKERS
; FILE REFERENCE: 10205 PSP
; CURRENT APPLICATION NUMBER: US/60/568,073
; CURRENT FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 1305
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1217
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-568-073-1217
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Query Match 44.2%; Score 1035.5; DB 7; Length 457;
Best Local Similarity 46.3%; Pred No. 2.8e-81;
Matches 216; Conservative 68; Mismatches 144; Indels 39; Gaps 12;
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QY 1 MRTLTP-PALLTC-----WLLAPVNS-----IHPECRFHLEIOBEETKCAELLRSTQEX 48
Db 1 MRPPSPUPARWLCVLGALAWALGAGQAARLQEECDYVQMIEVQHKQCLUEAQLNET 60
QY 49 HKACSGWMDNITCWRPANVGETVTPCPKVPNSFYKAG-NISKNTSDGMSFTFP-DFV 106
Db 61 -IGCSKMDNITCWPATPRGQVWVLAACPLIFKLFSSIQGRNVRSCTDEGWTLEPGYP 119
QY 107 DACGYSDEPE---DESKITFYILVKAITYLGVSVLSMSLATGSIILCLFRKLHCTRYIHL 163
Db 120 IACGLDDKAASLDEQQTWTFYGSVKTGYTIGVGLSLATLLVATALLSLFRKLHCTRYIHM 179
QY 164 NLFLSFILRAISVLVKDDVLYSSSTLHCPDPQSPSWGCKLSLVFLQYCI MANFFWLLVE 223
Db 180 HLFISFILRAAAVFIKDALFDSGESDQCE---GSVCKAAWVFFQYCVMANFFWLLVE 236
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QY 224 GLYLHTLL-VAMLPERRCFLAYLIGWGLPTVCIGAMTAARLYLEDTCGWDNDHSPVW 282
Db 237 GLYLHTLLAVSFYFERRKYFWGYIILIGWGPSTFTMVWVTIARIHFEDYGCWDTINSSL-WW 295
QY 283 VIRIPILISIIIVNFVLFISIIRILLOKLTSPDVGNDSQYKRLAKSTLLIPLFGVHYM 342
Db 296 IIKGPILTSILVNFILFICIIRILLOKLRPPDIRKSDSPYSRLARSTLLIPLFGVHYI 355
QY 343 VFVFPISISKYQILFELCLGSPQGLVAVLYCFLNSEVQCELRKWR----- 391
Db 356 MFAPFPDNFXDEKVMFELVVGSGFQGVVAILYCFLNGEVQAEELRRKWRWHLQGVLGWN 415
QY 392 SRCPTPSASRDYRVCGSFSRNGSEGAQPHRGSRASQFLQETSVI 438
Db 416 PKYRHPGGSGNGATCSTQVSM-----LTRVSPGARRSSSFQAEVSLV 457
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Search completed: June 22, 2004, 09:03:58  
Job time : 22 secs